

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:36:04 ; Search time 112.991 Seconds
(without alignments)
521.183 Million cell updates/sec

Title: us-10-058-069-7_COPY_20_134

Perfect score: 605
Sequence: 1 QVQLVQSGAEVHPGASVKI.....CTRSLNMAVWGQTLVTSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : UNIPROT_03

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	459.5	76.0	487	2	Q65ZL2
2	453.5	75.0	465	2	Q6PJB2
3	443	73.2	473	2	Q9D8L4
4	434	71.7	481	2	Q91WT1
5	420	69.4	489	2	Q8VCX4
6	417	68.9	120	1	HV03_MOUSE
7	417	68.9	480	2	Q8K0Z4
8	415	68.6	614	2	Q7TWT6
9	414.5	68.5	109	2	Q9JLT5
10	414.5	68.5	145	2	Q924Q9
11	414	68.4	140	1	HV02_MOUSE
12	414	68.4	146	2	Q924Q3
13	412	68.1	244	2	Q65ZC8
14	411.5	68.0	482	2	Q8K172
15	410	67.8	140	2	Q924P8
16	410	67.8	142	2	Q924Q1
17	410	67.8	464	2	Q6PF95
18	409.5	67.7	145	2	Q924Q6
19	409.5	67.7	145	2	Q924R4
20	408	67.4	140	2	Q924R2
21	406.5	67.2	143	2	Q924R0
22	405.5	67.0	124	2	Q9UL92
23	405.5	67.0	613	2	Q8VCX7
24	405	66.9	134	2	Q65ZR6
25	404.5	66.9	139	2	Q924R5
26	403.5	66.7	145	2	Q924R1
27	403.5	66.7	463	2	Q99LC4
28	402.5	66.5	518	2	Q6N030
29	402	66.4	146	2	Q924R8
30	401.5	66.4	137	2	Q924R6
31	401.5	66.4	139	1	HV07_MOUSE

ALIGNMENTS

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RESULT 1
Q65ZL2 PRELIMINARY; PRT; 487 AA.
AC Q65ZL2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE FV/M4.
GN Name=M4-IFN-<tau>;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96272580; PubMed=8698499;
RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RL antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00409; IGV; 3.
DR SMART; SM00408; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_LIKE; 4.
SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match 76.0%; Score 459.5; DB 2; Length 487;
Best Local Similarity 77.2%; Pred. No. 1.4e-38;
Matches 88; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 60
DB 20 QVQLQSDAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDIKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMYWGQGLTVTVS 114
DB 80 NEKFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMYWGQGLTVTVS 132

RESULT 2
Q6PJB2 PRELIMINARY; PRT; 465 AA.
AC Q6PJB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -.
DR HSSP; P01865; 1KBS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4B8DB3E21 CRC64;

Query Match 75.0%; Score 453.5; DB 2; Length 465;
Best Local Similarity 75.0%; Pred. No. 5.4e-38;
Matches 87; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDFKY 60
DB 20 QVQLQSDAEVVKPGASVKISCKASGYTFNSYIMHWKQNPQORLEWIGYFSPYNDTRK 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMYWGQGLTVTVS 115
DB 80 NEKFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMYWGQGLTVTVS 135

RESULT 3
Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:181060009 product:immunoglobulin heavy chain 6 (heavy
DE chain of IgM), full insert sequence.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
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Matches 85; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDDFKY 60
Db 20 QVQLVQSGDELVKPGASVKISKASGYTFTSYIIHWVKQRPQGLVIGWIYFGDNTKY 79

QY 61 NERFKGKATLTADTSGASTAYVELSLRSRSDTAVYFCTRSLNMA--YWGQGLTVTVSS 115
Db 80 NEKFKGKTLTADKSSSTAYMFLSLTSRSDSAVYFCTRGCGWAFDYWGQGLTVTVSS 136

RESULT 5
QBVCX4
ID QBVCX4 PRELIMINARY; PRT; 489 AA.
AC QBVCX4;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC018322; AAH18322.1; -.
DR HSSP; P01751; 1A6W.
DR MGD; MGI:96486; Igh-VJ558.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN.2.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFBF2C CRC64;

Query Match 69.4%; Score 420; DB 2; Length 489;
Best Local Similarity 63.2%; Pred. No. 1.6e-34;
Matches 79; Conservative 18; Mismatches 18; Indels 10; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDDFKY 60
Db 20 QVQLVQSGDELVKPGASVKISKASGYTFTSYIIHWVKQRPQGLVIGWIYFGDNTKY 79

QY 61 NERFKGKATLTADTSGASTAYVELSLRSRSDTAVYFCTRSLN-----MAYWGQGLT 110
Db 80 NEKFKDADTLTADKSTTVMDSLTSDSAVYFCARHEDRGNYDGLAWFVYWGQGLT 139
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QY 111 VTSS 115
Db 140 VTSA 144

RESULT 6
HV03 MOUSE
ID HV03 MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Igh heavy chain V region 36-65.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Geter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotypic response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032 (1982).
CC - MISCELLANEOUS: From analysis of the sizes of several other
CC differentiated genes that hybridize to this one, the authors
CC conclude that all of these V regions have rearranged to the same J
CC segment, JH2.
CC - SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PDB; 1UFO; X-ray; H=1-120.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 111
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 68.9%; Score 417; DB 1; Length 120;
Best Local Similarity 66.7%; Pred. No. 6.6e-35;
Matches 80; Conservative 14; Mismatches 20; Indels 6; Gaps 1;

QY 2 VQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDDFKY 61
Db 1 VQLVQSGAELVRAGSVKMSKASGYTFTSYGINNVKQRPQGLVIGWIYFGDNTKY 60

QY 62 ERFKGAATLTADTSGASTAYVELSLRSRSDTAVYFCTRSLNMA-----YWGQGLTVTVSS 115
Db 61 ERFKGTTLTVDKSSSTAYMQLRSLTSDSAVYFCARSVYGGSYFYWGQGLTVTVSS 120

RESULT 7
QBK024
ID QBK024 PRELIMINARY; PRT; 480 AA.
AC QBK024;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettemann M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleja U., Smallos D.E., Schnorrer A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RD Strausberg R.;
RE Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RF ENBL; BC053409; AAHS3409.1; -.
RG HSSP; PO1820; IG7U.
RH InterPro; IPR007110; Ig-like.
RI InterPro; IPR003597; Ig cl.
RJ InterPro; IPR003006; Ig_MHC.
RK InterPro; IPR003596; Ig_v.
RL Pfam; PF07654; C1-set; 4.
RM SMART; SM00406; IGV; 1.
RS PROSITE; PS00835; IG_LIKE; 5.
RQ PROSITE; PS00230; IG_MHC; UNKNOWN_3.
RY SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;
Query Match 68.6%; Score 415; DB 2; Length 614;
Best Local Similarity 68.9%; Pred. NO. 6.5e-34;
Matches 82; Conservative 12; Mismatches 21; Indels 4; Gaps 1;
QY 1 QVQLVSGAEVKPGASVKISCKASYTFTHAIHWKPNQPGRLEWIGYFSQGNDPFKY 60
Db |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
20 QVQLQSGLVELKPGASVKISCKASYAFSSSMNWKPKRPKGLEIWGIRVFQGDGTNY 79
QY 61 NERFKGKATLTADTSTAYVELLSURSEDYAVFYCTR---SLNWAYMQGGTLVTVS 115
Db |::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
80 NGKFPGKATLTADKSSTAYMLSSLTSSEDSAVYFCARDYGSSRYFAVMQQGLTVTVA 138
RESULT 9
Q9JL75 PRELIMINARY; PRS; 109 AA.
AC OSJUL75; ID 09JL75; AC OSJUL75; ID 09JL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090; RN [1];
RX SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.128/JA.68.L.5803-5808.2000;
RX Maikael S., Lisao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
RD ENBL; AFZ06031; AAF69329.1; -.
DR PIR; A30502; A30502.
DR PIR; PH0989; PH0989.
DR PIR; PH0990; PH0990.
DR PIR; PH0991; PH0991.
DR PIR; PH0992; PH0992.
DR PIR; PH0993; PH0993.
DR PIR; PH0994; PH0994.
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DR PIR; PH0995; PH0995.
DR PIR; PH1094; PH1094.
DR PIR; PH1096; PH1096.
DR PIR; S26312; S26312.
DR PIR; S26313; S26313.
DR HSSP; P01751; 1NQ8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109 1
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBP936A6 CRC64;

Query Match
Best Local Similarity 68.5%; Score 414.5; DB 2; Length 109;
Matches 78; Conservative 12; Mismatches 16; Indels 3; Gaps 1;

QY 10 EVVKPGASVKISCKASGYTFTDTHAIHWVKONPGQRLIEWIGYFSPGNDDFKYGKAT 69
DB 1 ELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTYKNEKFKGKAT 60

QY 70 LTADTSASTAYVELSLRSEDTSVYFCTSLN---MAYWGQGLTVTVSS 115
DB 61 LTSDKSSSTAYMELSLTSDSAVYCARDGNRYGRFDYWGQGLTVTVSS 109

RESULT 10
Q924Q9 PRELIMINARY; PRT; 145 AA.
ID Q924Q9
AC Q924Q9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vh186.2-D-J-C mu protein (Fragment).
GN Names:Vh186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067791; BAB63276.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 11
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FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match
Best Local Similarity 68.5%; Score 414.5; DB 2; Length 145;
Matches 81; Conservative 12; Mismatches 22; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKONPGQRLIEWIGYFSPGNDDFKY 60
DB 1 QVQLQPGAEVVKPGASVKISCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTYKNEKFKGKAT 60

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDTSVYFCTSLN---NMAVWGQGLTVTVSS 115
DB 61 NEKFKGKATLTVDKPSSTAYMQLSLTSDSAVYCARSLITTYVANDYWGQGLTVTVSS 120

RESULT 11
HV02 MOUSE STANDARD; PRT; 140 AA.
ID HV02 MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00493; AAA38128.1; -.
CC PIR; A94264; HVMSG7.
CC HSSP; P01747; 1JFQ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PSS0835; IG_LIKE; 1.
CC Hybridoma; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 Ig heavy chain V region 93G7.
FT DOMAIN 20 139 Ig-like.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match
Best Local Similarity 68.4%; Score 414; DB 1; Length 140;
Matches 79; Conservative 15; Mismatches 21; Indels 6; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKONPGQRLIEWIGYFSPGNDDFKY 60
DB 20 EVQLQSGAEVLRAGSVKMSCKASGYTFTSYGINWVKQKPGQGLEWIGYINPYNGYIN 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDTSVYFCTSLN---SLNMAVWGQGLTVTVSS 114
DB 80 NEKFKGKATLTVDKSSSTAYMQLSLTSDSAVYFCARSHYGGSYDFDYWGQGLTVTVSS 139
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Qy 115 S 115
Db 140 S 140

RESULT 12
Q924Q3
ID Q924Q3 PRELIMINARY; PRT; 146 AA.
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
GN Name=VHI86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (JUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067797; BAB63282.1; -.
DR PIR; F28833; F28833.
DR PIR; F39332; F39332.
DR PIR; F11105; P11105.
DR PIR; P11108; P11108.
DR PIR; P11114; P11114.
DR PIR; P11118; P11118.
DR PIR; P11119; P11119.
DR PIR; P11125; P11125.
DR PIR; P11126; P11126.
DR PIR; P11128; P11128.
DR PIR; P11129; P11129.
DR PIR; P11131; P11131.
DR PIR; P11134; P11134.
DR PIR; P11137; P11137.
DR PIR; P11139; P11139.
DR PIR; P11142; P11142.
DR PIR; P11144; P11144.
DR PIR; P11147; P11147.
DR PIR; P11149; P11149.
DR PIR; P11150; P11150.
DR PIR; P11151; P11151.
DR PIR; P11152; P11152.
DR PIR; P11153; P11153.
DR HSP; P01751; I1A6W.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 146 146
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16136 MW; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match 68.4%; Score 414; DB 2; Length 146;
Best Local Similarity 66.9%; Pred. No. 1.7e-34;
Matches 81; Conservative 12; Mismatches 22; Indels 6; Gaps 1;

Qy 1 QVOLVQSGAEVVKPGASVKISCKASGYTPTDTHAIHWKQNPGRLEWIGYFSPGNDDFKY 60
Db 1 QVOLVQSGAEVVKPGASVKISCKASGYTPTDTHAIHWKQNPGRLEWIGYFSPGNDDFKY 60
Qy 61 NERFKGKATLTADTSASTAYVELSSLRSEDATVYFCTRSI-----NMAYWGQGLTVTVS 114
Db 61 NERFKGKATLTADTSASTAYVELSSLRSEDATVYFCTRSI-----NMAYWGQGLTVTVS 114
Qy 115 S 115
Db 121 S 121

RESULT 13
Q8K172
ID Q8K172 PRELIMINARY; PRT; 482 AA.
AC Q8K172;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RESULT 17
Q6PF95 PRELIMINARY; PRT; 464 AA.
AC DT 05-JUL-2004 (TrEMBLrel. 27, Created)
AT Q6PF95;
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RA STRAIN=CZECH II; TISSUE=Mammary tumor;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC057672; AAH57672.1; -.
DR HSSP; P01865; IKB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51096 MW; 5B837464D85A1888 CRC64;

Query Match 67.8%; Score 410; DB 2; Length 464;
Best Local Similarity 67.8%; Pred. No. 1.6e-33;
Matches 78; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
DB 20 QVQLKQSGAEVLPKPGASVKLSCKASGYFTSYWIHWVKQSGQGLEWIRIYFGTSTYY 79

QY 61 NERFKGKATLTADTSASTAYVELSSLASEDTAVYFCTRSLNMAVWGQGLTVTVSS 115
DB 80 NERFKGKATLTADKSSSTAFQWLSLSKSDSAVYFCAVGYDALYWGQGLTVTVSS 134

RESULT 18
Q924Q6 PRELIMINARY; PRT; 145 AA.
ID Q924Q6
AC Q924R4 PRELIMINARY; PRT; 145 AA.
AD Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 25, Last sequence update)
DE Vhl186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB067794; BAB63279.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; IAGW.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 145
FT NON_TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 67.7%; Score 409.5; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 4.8e-34;
Matches 80; Conservative 12; Mismatches 23; Indels 5; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
DB 1 QVQLQPGAEVLPKPGASVKLSCKASGYFTSYWVHWVKQPGGLEWIGRIDPNSGGTKY 60

QY 61 NERFKGKATLTADTSASTAYVELSSLASEDTAVYFCTRS-----LNMAVWGQGLTVTVSS 115
DB 61 NERFKSKATLTVDKPSSTAYMQLSSLTSDSAVYVCARSTLSHYVADYWGQGLTVTVSS 120

RESULT 19
Q924R4 PRELIMINARY; PRT; 145 AA.
ID Q924R4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 25, Last sequence update)
DE Vhl186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```


RESULT	23	Q8VCX7	PRELIMINARY;	PRT;	613 AA.
AC	Q8VCX7	Q8VCX7			
DC	Q8VCX7	Q8VCX7			
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE		Igh-6 protein.			
GN		Name=Igh-6;			
OS		Mus musculus (Mouse).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX		NCBI_Taxid=10090;			
RN		[1]			
RP		SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N;	TISSUE=Salivary gland;			
RC	MEDLINE=22388257;	PubMed=12477932;	DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L.,	Feingold E.A.,	Grouse L.H.,	Derge J.G.,	
RA	Klausner R.D.,	Collins F.S.,	Wagner L.,	Shenmen C.F.,	Schuler G.D.,
RA	Altschul S.F.,	Zeberg B.,	Buetow K.H.,	Schaefer C.F.,	Bhat N.K.,
RA	Hopkins R.F.,	Jordan H.,	Moore T.,	Max S.I.,	Wang J.,
RA	Diatchenko L.,	Marusina K.,	Farmer A.A.,	Rubin G.M.,	Hong L.,
RA	Strapleton M.,	Soares M.B.,	Bonaldo M.P.,	Casaavant T.L.,	Scheetz T.E.,
RA	Brownstein M.J.,	Ustin T.B.,	Toshiyuki S.,	Carninci P.,	Prange C.,
RA	Raha S.,	Loquellano N.A.,	Peters G.J.,	Abrahamson R.D.,	Mullahy S.J.,
RA	Bosak S.A.,	McEwan P.J.,	McKernan K.J.,	Malek J.A.,	Gunaratne P.H.,
RA	Richards S.,	Worley K.C.,	Hale S.,	Garcia A.M.,	Gay L.J.,
RA	Villalon D.K.,	Muzny D.,	Sodergren E.J.,	Lu X.,	Gibbs R.A.,
RA	Fahey J.,	Helton E.,	Kettenan M.,	Madan A.,	Rodrigues S.,
RA	Whiting M.,	Madan A.,	Young A.C.,	Shevchenko Y.,	Bouffard G.G.,
RA	Blakesley R.W.,	Touhman J.W.,	Green E.D.,	Dickson M.C.,	
RA	Rodriguez A.C.,	Grimwood J.,	Schmutz J.,	Myers R.M.,	Butterfield Y.S.,
RA	Krzywinski M.I.,	Skaleka U.,	Smailus D.E.,	Schnerch A.,	Schein J.E.,
RA	Jones S.J.,	Marra M.A.			
RT		"Generation and initial analysis of more than 15,000 full-length human			
RT		and mouse cDNA sequences."			
RL		Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RL		[2]			
RP		SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N;	TISSUE=Salivary gland;			
RC	Strausberg R.,				
RL	Submitted (DEC-2001)	to the EMBL/GenBank/DBDJ databases.			
DR	EMBL;	BC018315; RAH18315.1; -.			
DR	PIR;	C30562; C30562.			
DR	HSSP;	P01751; 1A6W.			
DR	MGD;	MGI:96448; Igh-6.			
DR	GO;	GO:0019815; C:B-cell receptor complex; IDA.			
DR	GO;	GO:0009897; C:external side of plasma membrane; IDA.			
DR	GO;	GO:0042571; C:immunoglobulin complex, circulating; IDA.			
DR	GO;	GO:0003823; P:antigen binding; IDA.			
DR	GO;	GO:0030333; P:antigen processing; IDA.			
DR	GO;	GO:0045022; P:early endosome to late endosome transport; IDA.			
DR	GO;	GO:0010684; P:innate defense mechanism (sensu Vertebrata); IDA.			
DR	GO;	GO:0050871; P:positive regulation of B-cell activation; IDA.			
DR	GO;	GO:0030890; P:positive regulation of B-cell proliferation; IDA.			
DR	GO;	GO:0045807; P:positive regulation of endocytosis; IDA.			
DR	Pfam;	PF07654; Cl-set; 4.			
DR	SMART;	SM00406; IGV; 1.			
DR	PROSITE;	PS00835; IG_LIKE; 5.			
DR	PROSITE;	PS00290; IG_MHC5; UNKNOWN 3.			
SQ	SEQUENCE	613 AA; 67855 MW; 41A9384DD4C22862 CRC64;			
	Query Match	67.0%;	Score 405.5;	DB 2;	Length 613;
	Best Local Similarity	66.9%;	Pred. No. 6.1e-33;		
	Matches	79;	Conservative	13;	Mismatches 23; Indels 3; Gaps 1
QY	1	QVQLVQSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQRLEWIGYFSPGNDDPKY	60		
DB	20	QVQLQSGAEELMKPGASVKISCKATGYTFSYIEWVKQRPGHGLEWIGELPQSGSTNY	79		
QY	61	NERPFGKATLTADTSASTAYVELSLRSEDYAVYFCTRSIMNAY---WGQGLTVVSS	115		
DB	80	NEKFGKATFTADTSNTAYVOLSLTSEDYAVYCARLRGWYFDVWGAGTIVVSS	137		

```
RESULT 24
Q52R6
ID Q652R6 PRELIMINARY; PRT; 134 AA.
AC Q652R6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ab 126-33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=91237115; PubMed=1709665;
RX Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Junctional diversity of H and L chains allows the coexpression of two
mutually exclusive idiotopes (Idi104 and Idi558).";
RL J. Immunol. 146:4024-4030(1991).
DR EMBL; M74139; AAA37776.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match
Best Local Similarity 66.9%; Score 405; DB 2; Length 134;
Matches 76; Conservative 18; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPGORLEWIGYFSPGNDDPKY 60
DB 18 EVQLQSGPELVKPGASVKMSCKASGYTFTDYMKVKQSPGKSLWIGDINPNNGTSY 77
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMA--YWGQGLTVTVSS 115
DB 78 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYCARDYSYVFDYWGQGLTVTVSS 134

RESULT 25
Q24R5
ID Q924R5 PRELIMINARY; PRT; 139 AA.
AC Q924R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067784; BAB63269.1; -.
DR PIR; PH1137; PH1137.
DR HSSP; P01751; 1A6V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 139
SQ SEQUENCE 139 AA; 15221 MW; 8491E2F85614736A CRC64;

Query Match
Best Local Similarity 66.9%; Score 404.5; DB 2; Length 139;
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Best Local Similarity 67.8%; Pred. No. 1.5e-33;
Matches 78; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKONPGORLEWIGYFSPGNDDPKY 60
DB 1 QVQLQQPGAEIVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNFGGTYKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRLNMA--YWGQGLTVTVSS 115
DB 61 NEKFKSRATLTVDKPSSTAYMQLSLTSDSAVYCA-LLAEAYWGQGLTVTVSA 114

Search completed: July 25, 2005, 08:00:06
Job time : 114.991 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:52:16 ; Search time 24.607 Seconds
(without alignments)
449.666 Million cell updates/sec

Title: US-10-058-069-7_COPY_20_134

Perfect score: 605

Sequence: 1 QVLVQSGAEVVKPGASVKI.....CTRSLNMAVWGQTLVTSS 115

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_29.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470.5	77.8	133	2	PC1155
2	456	75.4	138	2	S21810
3	447	73.9	246	2	S38950
4	447	73.9	446	2	S40295
5	444	73.4	119	2	S20640
6	436.5	72.1	469	2	S37483
7	435.5	72.0	131	2	S66537
8	433.5	71.7	112	2	A30502
9	432.5	71.5	115	2	A54378
10	430.5	71.2	118	2	S38717
11	428.5	70.8	474	1	G2MS11
12	426	70.4	119	2	E30562
13	423.5	70.0	118	2	S36265
14	422.5	69.8	135	2	A30577
15	422.5	69.8	139	2	PS0024
16	422	69.8	125	2	S20639
17	422	69.8	140	2	PH1484
18	421	69.6	119	2	C30562
19	421	69.6	123	2	F48677
20	419	69.3	138	2	E32513
21	419	69.3	140	2	PH1482
22	419	69.3	140	2	S04575
23	418.5	69.2	120	2	G28195
24	418.5	69.2	122	2	S32185
25	418.5	69.2	139	2	A27609
26	417	68.9	119	2	S45714
27	416	68.8	119	2	D30562
28	416	68.8	121	2	A26405
29	416	68.8	123	2	G48677

30	416	68.8	142	2	A32483	Ig heavy chain V r
31	415	68.6	117	2	S09960	Ig heavy chain V-D
32	414.5	68.5	144	2	B30502	Ig heavy chain V r
33	414	68.4	116	2	S55542	Ig heavy chain V r
34	414	68.4	140	1	HVMSG7	Ig heavy chain pre
35	413.5	68.3	117	2	S25176	Ig heavy chain V r
36	413	68.3	118	2	S38565	Ig heavy chain V r
37	413	68.3	123	2	E48677	Ig heavy chain V-D
38	411.5	68.0	112	2	PL0245	Ig heavy chain V r
39	411.5	68.0	120	2	S41394	Ig heavy chain V r
40	411.5	68.0	120	2	F28195	Ig heavy chain V r
41	411.5	68.0	120	2	B22769	Ig heavy chain V r
42	410.5	67.9	135	2	S49530	anti-Sm antibody V
43	410	67.8	121	2	A21854	Ig heavy chain V r
44	408	67.4	117	2	JC2269	PL7-6 antibody hea
45	408	67.4	123	2	D33548	Ig heavy chain V-1
46	408	67.4	136	2	PL0208	Ig heavy chain pre
47	407.5	67.4	118	2	S37201	Ig heavy chain V r
48	407	67.3	109	2	PH1001	Ig heavy chain V r
49	407	67.3	140	2	PH1488	Ig heavy chain V r
50	405.5	67.0	104	2	PH1665	Ig heavy chain V r
51	405	66.9	111	2	PH0992	Ig heavy chain V r
52	405	66.9	118	2	PL0231	Ig heavy chain V r
53	405	66.9	123	2	S20646	Ig heavy chain V r
54	404.5	66.9	141	2	A32276	Ig heavy chain pre
55	403.5	66.7	110	2	PL0244	Ig heavy chain V r
56	403.5	66.7	110	2	PH0995	Ig heavy chain V r
57	403.5	66.7	116	2	S53751	Ig heavy chain (an
58	403.5	66.7	136	2	JL0077	Ig heavy chain pre
59	403	66.6	109	2	PH0989	Ig heavy chain V r
60	403	66.6	121	2	A30551	Ig heavy chain V r
61	403	66.6	140	2	PH1489	Ig heavy chain V r
62	402	66.4	111	2	PH0994	Ig heavy chain V r
63	402	66.4	115	2	A56700	Ig heavy chain (an
64	402	66.4	117	2	S19966	Ig heavy chain V r
65	402	66.4	121	2	S19969	Ig heavy chain V r
66	402	66.4	140	2	PH1498	Ig heavy chain V r
67	401.5	66.4	112	2	S26473	Ig heavy chain V r
68	401.5	66.4	117	2	S55541	Ig heavy chain V r
69	401.5	66.4	119	2	A24672	Ig heavy chain pre
70	401.5	66.4	137	2	F29380	Ig heavy chain pre
71	401.5	66.4	139	1	MEWS18	Ig heavy chain pre
72	401.5	66.4	287	4	PC4402	pelB leader/Ig hea
73	401	66.3	111	2	PH0993	Ig heavy chain V r
74	400	66.1	123	2	B30560	Ig heavy chain V r
75	399.5	66.0	126	2	S31930	Ig gamma chain pre
76	399	66.0	109	2	PH1096	Ig heavy chain V r
77	399	66.0	111	2	PH0990	Ig heavy chain V r
78	399	66.0	117	2	S18553	Ig heavy chain V r
79	398.5	65.9	141	2	JL0076	Ig heavy chain pre
80	398	65.8	109	2	PH1094	Ig heavy chain V r
81	398	65.8	119	2	PL0089	Ig heavy chain V r
82	397.5	65.7	128	2	I37267	Ig heavy chain V r
83	397	65.6	109	2	PH0997	Ig heavy chain V r
84	397	65.6	119	2	S19964	Ig heavy chain V r
85	397	65.6	135	2	PH1493	Ig heavy chain V r
86	396.5	65.5	114	2	PH1667	Ig heavy chain V r
87	396.5	65.5	120	2	S31999	Ig heavy chain V r
88	396.5	65.5	123	2	S60067	Ig heavy chain V r
89	396.5	65.5	135	2	S00057	Ig heavy chain pre
90	396	65.5	119	2	PH1518	Ig heavy chain V r
91	395.5	65.4	118	2	PH1666	Ig heavy chain V r
92	395.5	65.4	118	2	C30560	Ig heavy chain V r
93	395.5	65.4	128	2	C37267	Ig heavy chain pre
94	395.5	65.4	137	2	E29380	Ig heavy chain V r
95	395	65.3	117	2	S03305	Ig heavy chain V r
96	395	65.3	127	2	S34014	Ig heavy chain V r
97	395	65.3	148	2	S29257	Ig heavy chain V r
98	394.5	65.2	151	2	PL0011	Ig heavy chain pre
99	394.5	65.2	124	2	S19665	Ig heavy chain V r
100	394.5	65.2	140	2	S09216	Ig heavy chain pre

ALIGNMENTS

RESULT 1

PC1155
Ig heavy chain precursor V region (B72.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1155
R:Whittle, N.; Adair, J.; Lloyd, C.; Jenkins, L.; Devine, J.; Schlom, J.; Raubitschek, A.
Protein Eng. 1, 499-505, 1987
A:Title: Expression in COS cells of a mouse-human chimaeric B72.3 antibody.
A:Reference number: PC1155; MUID:89220990; PMID:3508296
A:Accession: PC1155

A:Molecule type: mRNA
A:Residues: 1-133 <WHI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-133/Product: Ig heavy chain V region (B72.3) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 470.5; DB 2; Length 133;
Best Local Similarity 78.3%; Pred. No. 2.6e-36;
Matches 90; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWAKQKPGQGLEWIGYISPGNDDIKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSRSDTAVYFCTR--SLNWAYWQOGLTVTVSS 115
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYFCRKYSGYGHWQOGLTVTVSS 133

RESULT 2

S21810
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21810
R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
submitted to the EMBL Data Library, January 1991
A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain
A:Reference number: S21810
A:Accession: S21810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-138 <OST>
A:Cross-references: EMBL:X56936; NID:G54163; PIDN:CAA40257.1; PID:G54164
C:Genetics:
A:introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 456; DB 2; Length 138;
Best Local Similarity 73.9%; Pred. No. 5.7e-35;
Matches 88; Conservative 12; Mismatches 15; Indels 4; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLQSGPELVKPGASVRIKASGYFTSYIHWKQRPQGLEWIGWIYPGNVNTKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSRSDTAVYFCTR----SLNWAYWQOGLTVTVSS 115
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSEDSAVYFCARNYSSGYLAYWQOGLTVTVSA 138

RESULT 3

S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)

C>Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Weisgerber, C.; Bit
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(G
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 447; DB 2; Length 246;
Best Local Similarity 72.6%; Pred. No. 7e-34;
Matches 85; Conservative 13; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 1 QIQLQSGPELVKPGASVKISKASGYTFTDYIHWKQRPQGLEWIGWIYPGSGNTKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSRSDTAVYFCTR--SLNWAYWQOGLTVTVSS 115
DB 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARGGKFAMDYWGQGTSTVTVSS 117

RESULT 4

S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
A:Cross-references: UNIPROT:Q99L25
C:Genetics:

A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CHI>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>

F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:122-96.144-199.261-321.367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224.227.229/disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 73.9%; Score 447; DB 2; Length 446;
Best Local Similarity 72.6%; Pred. No. 1.3e-33;
Matches 85; Conservative 13; Mismatches 17; Indels 2; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 1 QIQLQSGPELVKPGASVKISKASGYTFTDYIHWKQRPQGLEWIGWIYPGSGNTKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSRSDTAVYFCTR--SLNWAYWQOGLTVTVSS 115
DB 61 NEKFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARGGKFAMDYWGQGTSTVTVSS 117

RESULT 5

A;Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-131 <TSI>
A/Cross-references: EMBL:X89902; NID:g995869; PIDN:CAA61364.1; PID:g1103701
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 435.5; DB 2; Length 131;
Best Local Similarity 68.0%; Pred. No. 4.1e-33;
Matches 83; Conservative 14; Mismatches 18; Indels 7; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAIHVVKNPQORLEWIGYFSPGNDDPKY 60
:
Db 1 EVKLQESGAGLVKPGASVKMSKASGYFTSYVMHWVKQKPGGLEWIGYINPYNDGTKY 60
:
QY 61 NERFKGATLTADTSAAYVELSLRSRSDTAIFYCTRLN-----MAYWGQGLTVTV 113
:
Db 61 NEKFKGATLTDSKSSSTAYMELSSLTSEDSAVYYCARDYRDVWYYAMDYGQGLTVTV 120
:
QY 114 SS 115
||
Db 121 SS 122

RESULT 8
A30502
IG heavy chain V region (D44) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 03-Nov-1998 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Accession: A30502
J.Eilat, D.; Webster, D.M.; Rees, A.R.
R. Immunol. 141, 1745-1753, 1988
A/Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mice
A/Reference number: A30502; MUID:88315787; PMID:2457627
A/Accession: A30502
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-112 <EIL>
A/Cross-references: UNIPROT:Q9JL75
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 433.5; DB 2; Length 112;
Best Local Similarity 73.5%; Pred. No. 5.4e-33;
Matches 83; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAIHVVKNPQORLEWIGYFSPGNDDPKY 60
:
Db 1 EVQLQSGPELVKPGASVKMSKASGDTFTSSVMHWVKQKPGGLEWIGYINPYNDGTKY 60
:
QY 61 NERFKGATLTADTSAAYVELSLRSRSDTAIFYCTRLNMYWGQGLTVTV 113
:
Db 61 NEKFKGATLTDSKSSSTAYMELSSLTSEDSAVYYCARG-GFAIWGGQGLTVTV 112

RESULT 9
A54378
Ig heavy chain V region anti-triplex DNA - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: A54378
R.Agazie, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994
A/Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A/Reference number: A54378; MUID:94165109; PMID:7509814
A/Accession: A54378
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-115 <AGA>
A/Cross-references: GB:S68981; NID:g545744; PIDN:AAB30095.1; PID:g545745
A/Experimental source: spleen and myeloma cell line MOPC 315.43
A/Note: sequence inconsistent with nucleotide translation

A;Accession: E30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.4%; Score 426; DB 2; Length 119;
Best Local Similarity 68.9%; Pred. No. 2.8e-32;
Matches 82; Conservative 15; Mismatches 18; Indels 4; Gaps 1;

Qy 1 QVQLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQSGAEVVKPGASVKISCKATGYTFSSYIEWKQRPQGLWIGIFPGSGSTKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFCTRL--SINMAYWGQGLTVTVSS 115
Db 61 NERFKGKATLTADTSSTAYMQLSSLTSDSAVYCARHYGSSSFAYWGQGLTVTVSA 119

RESULT 13
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Giffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GPI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.08; Score 423.5; DB 2; Length 118;
Best Local Similarity 68.6%; Pred. No. 4.7e-32;
Matches 81; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

Qy 1 QVQLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLVSGAEVVKPGASVKISCKASGYTFGYMHWVQAPQGLWIMGNPSGNTY 60

Qy 61 NERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFCTRL--SINMAYWGQGLTVTVSS 115
Db 61 AOKFQGRVITRDTASTAYMELSSLSRSEDYAVYCARDPLSGYLDYWGQGLTVTVSS 118

RESULT 14
A30577
Ig heavy chain precursor V region (MRL10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
C;Accession: A30577
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof
J. Exp. Med. 161, 805-815, 1985
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela
A;Reference number: A30577; MUID:85159423; PMID:3920343
A;Accession: A30577
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <KOF>
A;Cross-references: GB:M37621
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 422.5; DB 2; Length 135;

Best Local Similarity 69.8%; Pred. No. 6.7e-32;
Matches 81; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

Qy 1 QVQLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 20 QVQLQSGAEVVKPGASVKISCKASGYTFSSYINWVWQRPQGLWIGIYFGSSSTNY 79

Qy 61 NERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFCTRL--NMAYWGQGLTVTVSS 115
Db 80 NERFKSKATLTVDTSSTAYMQLSSLTSDSAVYCARLVGGFAYWGQGLTVTVSA 135

RESULT 15
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C;Accession: PS0024
R;Margat, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A;Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A;Reference number: PS0023; MUID:89232725; PMID:3149944
A;Accession: PS0024
A;Molecule type: mRNA
A;Residues: 1-139 <MAR>
A;Experimental source: strain BALB/c
C;Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin; pyroglytamic acid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F;34-117/Domain: immunoglobulin homology <IMM>
F;20/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted

Query Match 69.8%; Score 422.5; DB 2; Length 139;
Best Local Similarity 69.2%; Pred. No. 6.9e-32;
Matches 83; Conservative 12; Mismatches 20; Indels 5; Gaps 1;

Qy 1 QVQLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 20 QVQLQSGAEVVKPGASVKISCKASGYTFYAWMHWKQRPQGLWIGIYINPTGYTEY 79

Qy 61 NERFKGKATLTADTSASTAYVELSSLSRSEDYAVYFCTRL-----NMAYWGQGLTVTVSS 115
Db 80 NQNFKDKATLTADKSSSTAYMQLSSLTSDSAVYCTRSYNYEGAMDYWGQGLTVTVSS 139

RESULT 16
S20639
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20639
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice react
A;Reference number: S20639
A;Accession: S20639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <LOS>
A;Cross-references: EMBL:X65004; NID:g52598; PIDN:CAA46137.1; PID:g52599
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 422; DB 2; Length 125;
Best Local Similarity 65.6%; Pred. No. 6.9e-32;
Matches 82; Conservative 12; Mismatches 19; Indels 12; Gaps 1;

Qy 1 QVQLVSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 EVQLQSGPELVKPGASVKISCKASGYTFSSYIMHWKQRPQGLWIGIYINLHNDGTY 60

Qy	61	NRKPGKATLTADTASTAYVELSLRSEDATVYECTRS-----LNWAYWGQ	108
Db	61	NRKPGKATLTSDKSSAYMELSLTSDSAVYCARVYNNYVLRSLLYAMDYWGQ	120
Qy	109	TLTVV 113	
Db	121	TSVTV 125	

RESULT 17
PH1484
Ig heavy chain V region (clones X7-3C5 and X7-3C5H) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1484; PH1497
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1484
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GIU>
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMW>

Query Match 69.8%; Score 422; DB 2; Length 140;
Best Local Similarity 66.1%; Pred. No. 7.7e-32;
Matches 80; Conservative 16; Mismatches 19; Indels 6; Gaps 1;

Qy	1	QVQLVQSGAEVVKPGASVKISKCKASGYTFTDTHAHHWVKQMPQQRLEWIGVYFSGNDDFKY	60
Db	20	EVQLQDSGAEFLVRGSSVKMSCKASGYTFTTNGINWVKRQPGQGLEWIGVINGPNDYIH	79
Qy	61	NERFGKATLTADTASTAYVELSLRSEDYAVFCTRSLNMA-----YWGQGLTVTS	114
Db	80	NKSPFKGKTTLTVDKSSYAYMQLRSLTSEDSAVYFCARSVYGGSYFDYWGQGTTLTWS	139

Qy	115 \$ 115
	—
D _b	140 \$ 140

RESULT 18
C30562
Ig heavy chain V region (27.7.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 09-Jul-2004
C/Accession: C30562
R/Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 898-899, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A/Reference number: A30562; MUID:89110066; PMID:2464031

A;Accession: C30362
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SIK>
A;Cross-references: UNIPROT:Q8VCX7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 421; DB 2; Length 119;
Best Local Similarity 68.1%; Pred. No. 8e-32;
Matches 81; Conservative 15; Mismatches 19; Indels 4; Gaps 1;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWVKQNPQGRLEWIGYFSPGNDFKY 60

Db	Qy
1	QVQLQQSGAELMKPGASVKISCKATGYTFSYIEWVKQRPGHGLEWIGETLPGGSTNY 60
61	NERPKGKATLTADTASATAYVELSRSRDATVYFCTR----SLNWKYQGCTLTVSS 115
61	NEKFKGKATFTADTSNTAYMOLSIITSEDSAVYTCARHYGSSSFAYWGQCTLTVSA 119

RESULT 19

F48677
Ig heavy chain V-D-J region (44.1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C/Accession: F48677
C/Rassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A/Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibodies
A/Reference number: A48677; MUID:94022404; PMID:8415731
A/Accession: F48677
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-133 <TAS>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 69.6%; Score 421; DB 2; Length 133;
Best Local Similarity 65.9%; Pred. No. 8.3e-32;
Matches 81; Conservative 14; Mismatches 20; Indels 8; Gaps 1

[illegible]

RESULT 20

E32513
Ig heavy chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-May-1990 #sequence_revision 31-Dec-1999
C/Accession: E32513
R/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duce
J. Clin. Invest. 82, 852-860, 1988
A/Title: Immunoglobulin kappa light chain variable region gene complex orga
A/Reference number: A94689; MUID:88331394; PMID:3138286
A/Accession: E32513
A/Molecule type: DNA
A/Residues: 1-138 <KOF>
A/Cross-references: GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:g196946
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.3%; Score 419; DB 2; Length 138;
Best Local Similarity 68.9%; Pred. No. 1.4e-31;
Matches 82; Conservative 12; Mismatches 21; Indels 4; Gaps 1

Qy	1	QVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWVKONQORLEWICYSPGNDDPKY	60
Db	20	QVQLQQPGAEVVKPGASVKISKASGYFTTSWIINWVKQPGGLEWIGNIYPGSSSTNY	79
Qy	61	NERFKGKATLTADTASTAYVELSLRSEDTSYFTCSRL-----NNAVYQGQTLVTVSS	115
Db	80	NKFKFSKATLTVDTSSTAYMQLSLLSDSDSVAVYCARRLRYVANDYWGQTSVTVSS	138

RESULT 21

PH1482
Ig heavy chain V region (clones 36-35[IG] and X7-TG) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1482; PH1495
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1482
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-140 <GU>
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 69.3%; Score 419; DB 2; Length 140;
Best Local Similarity 66.1%; Pred. No. 1.5e-31;
Matches 80; Conservative 15; Mismatches 20; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGORLEWIGYFSPGNDDFKY 60

Db 20 EVQLQSGAEVLRAGSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGVINGYTKY 79

QY 61 NERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSNLMA-----YWGQGLTVTS 114

Db 80 NERFKGKATLTVDKSSSTAYMQLSLTSDSAVYFCARSVYGVYFYWGQGLTVTS 139

QY 115 S 115

Db 140 S 140

RESULT 22

S04575
Ig heavy chain precursor V region (MRL-RF24) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C:Accession: S04575
R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
Eur. J. Immunol. 17, 91-95, 1987
A:Title: Molecular analysis of the murine lupus-associated anti-self response: involve
A:Reference number: S04573; MUID:87133856; PMID:3102255
A:Accession: S04575
A:Molecule type: mRNA
A:Residues: 1-140 <KOP>
A:Cross-references: EMBL:X14623; NID:952398; PIDN:CAA32776.1; PID:952399
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-140/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IM>

Query Match 69.3%; Score 419; DB 2; Length 140;
Best Local Similarity 67.8%; Pred. No. 1.5e-31;
Matches 82; Conservative 12; Mismatches 21; Indels 6; Gaps 1;

QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGORLEWIGYFSPGNDDFKY 60

Db 20 QVQLQSGAEVLRAGSVKMSCKASGYTFTSYGINWVKQRPQGLEWIGVINGYTKY 79

QY 61 NERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSNLMA-----LNMAYWGQGLTVTS 114

Db 80 NERFKGKATLTVEKSSSTAYVLESLRSLTSDSAVYFCARGPITGHYAMDYWGQGLTVTS 139

QY 115 S 115

Db 140 S 140

RESULT 23

G28195
Ig heavy chain V region (anti-haloperidol antibody B) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C:Accession: G28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: G28195
A:Molecule type: mRNA
A:Residues: 1-120 <SHE>
A:Cross-references: GB:M19772; NID:gl95520; PIDN:AAA38340.1; PID:gl95521
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IM>

Query Match 69.2%; Score 418.5; DB 2; Length 120;
Best Local Similarity 68.3%; Pred. No. 1.4e-31;
Matches 82; Conservative 13; Mismatches 20; Indels 5; Gaps 1;

QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGORLEWIGYFSPGNDDFKY 60

Db 1 QVQLQSGAEVLRAGSVKISCKASGYTFTSYIHWLQRPQGPQGWIGVINGYTKY 60

QY 61 NERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSNLMA-----YWGQGLTVTS 115

Db 61 NERFKGKATLTADKSSSTAYMQLSLTSDSAVYFCAREGSYEADYWGKGTTLTVSS 120

RESULT 24

S32185
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S32185
R:Izui, S.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <IZU>
A:Cross-references: EMBL:X70089; NID:g288247; PIDN:CAA49694.1; PID:g288248
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IM>

Query Match 69.2%; Score 418.5; DB 2; Length 122;
Best Local Similarity 66.4%; Pred. No. 1.4e-31;
Matches 81; Conservative 13; Mismatches 21; Indels 7; Gaps 1;

QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGORLEWIGYFSPGNDDFKY 60

Db 1 QVQLQSGAEVLRAGSVKISCKASGYTFTSYIHWKQRPQGPQGWIGVINGYTKY 60

QY 61 NERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSNLMA-----AYWGQGLTVTV 113

Db 61 TEKFKDKATLTADKSSSTAYMQLSLTSDSAVYFCARHSGISTVVGFRFAYWGXGTLVTA 120

QY 114 SS 115

Db 121 SA 122

RESULT 25

A27609
Ig heavy chain precursor V region (129) - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
 C:Accession: A27609
 R:Klein, D.; Niecupski, J.; Sirlin, S.; Stavnezer, J.
 J. Immunol. 140, 1676-1684, 1988
 A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
 A:Reference number: A27609; MUID:88154467; PMID:3126234
 A:Accession: A27609
 A:Molecule type: DNA
 A:Residues: 1-139 <KIE>
 A:Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 418.5; DB 2; Length 139;
 Best Local Similarity 66.7%; Pred. No. 1.6e-31;
 Matches 80; Conservative 16; Mismatches 19; Indels 5; Gaps 1;

QY	1	QVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY	60
		: : : : : : : :	
Db	20	EVQLQQSGPELVKPGASVKMSCKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY	79
		: : : : : : : :	
QY	61	NERFKGKATLTADTSASTAYVELSLRSEDYVYFCTR-----SLNMYWGQGLTVTVSS	115
		::: : : : : : : :	
Db	80	NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYCYARYSYSYAMDYWGQGLTVTVSS	139
		::: : : : : : : :	

Search completed: July 25, 2005, 08:13:44
 Job time : 26.607 secs


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85 447 73.9 117 16 US-10-729-441-76 Sequence 76, Appl
86 447 73.9 117 18 US-10-895-135-54 Sequence 54, Appl
87 447 73.9 119 17 US-10-763-424-60 Sequence 60, Appl
88 446.5 73.8 116 18 US-10-837-904-128 Sequence 128, App
89 446 73.7 483 16 US-10-679-820-122 Sequence 122, App
90 445.5 73.6 116 18 US-10-837-904-126 Sequence 126, App
91 445 73.6 115 9 US-09-999-025-3 Sequence 3, Appli
92 445 73.6 115 9 US-09-999-025-11 Sequence 11, Appl
93 445 73.6 115 9 US-09-999-040-3 Sequence 3, Appli
94 445 73.6 115 9 US-09-999-040-11 Sequence 11, Appl
95 445 73.6 115 10 US-09-998-817-3 Sequence 3, Appli
96 445 73.6 115 10 US-09-998-817-11 Sequence 11, Appli
97 445 73.6 115 10 US-09-999-021-3 Sequence 3, Appli
98 445 73.6 115 10 US-09-999-021-11 Sequence 11, Appli
99 445 73.6 115 14 US-10-040-997-3 Sequence 3, Appli
100 445 73.6 115 14 US-10-040-997-11 Sequence 11, Appl

ALIGNMENTS

US-10-255-478-76
; Sequence 76, Application US/10255478
; Publication No. US20030165498A1
; GENERAL INFORMATION:
; APPLICANT: Mezees, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kaehmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padlan, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; TITLE OF INVENTION: Capable of Binding to TAG-72
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/10/255,478
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/08/961,309
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 08/261,354
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: US 07/964,536
; PRIOR FILING DATE: 1992-10-20
; PRIOR APPLICATION NUMBER: US 07/510,697
; PRIOR FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 76
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: HuCC49 VH
; LOCATION: 1..115
; OTHER INFORMATION: Humanized CC49 heavy chain variable region with 21/28'CL VH FRs
; FEATURE:
; NAME/KEY: 21/28'CL FR1
; LOCATION: 1..30
; OTHER INFORMATION: Human 21/28'CL heavy chain variable region FR1
; FEATURE:
; NAME/KEY: CC49 VH CDR1
; LOCATION: 31..35
; OTHER INFORMATION: Murine CC49 heavy chain variable region CDR1
; FEATURE:
; NAME/KEY: 21/28'CL FR2
; LOCATION: 36..49
; OTHER INFORMATION: Human 21/28'CL heavy chain variable region FR2
; FEATURE:
; NAME/KEY: CC49 VH CDR2
; LOCATION: 50..66
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; OTHER INFORMATION: Murine CC49 heavy chain variable region CDR2
; FEATURE:
; NAME/KEY: 21/28'CL FR3
; LOCATION: 67..98
; OTHER INFORMATION: Human 21/28'CL heavy chain variable region FR3
; FEATURE:
; NAME/KEY: CC49 VH CDR3
; LOCATION: 99..104
; OTHER INFORMATION: Murine CC49 heavy chain variable region CDR3
; FEATURE:
; NAME/KEY: 21/28'CL FR4
; LOCATION: 105..115
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US-10-255-478-76

Query Match 100.0%; Score 605; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWVKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWVKQNPQORLEWIGYFSPGNDDPKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDPAVYFCTSLNMAWYGQGTSLTVSS 115
Db 61 NERFKGKATLTADTSASTAYVELSLRSEDPAVYFCTSLNMAWYGQGTSLTVSS 115

RESULT 2
US-09-999-025-1
; Sequence 1, Application US/09999025
; Publication No. US20020183497A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,025
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
; OTHER INFORMATION: Humanized CC49 heavy chain variable region with 21/28'CL VH FRs
; FEATURE:
; NAME/KEY: 21/28'CL FR1
; LOCATION: 1..30
; OTHER INFORMATION: Human 21/28'CL heavy chain variable region FR1
; FEATURE:
; NAME/KEY: CC49 VH CDR1
; LOCATION: 31..35
; OTHER INFORMATION: Murine CC49 heavy chain variable region CDR1
; FEATURE:
; NAME/KEY: 21/28'CL FR2
; LOCATION: 36..49
; OTHER INFORMATION: Human 21/28'CL heavy chain variable region FR2
; FEATURE:
; NAME/KEY: CC49 VH CDR2
; LOCATION: 50..66
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US-09-999-025-10
; Sequence 10, Application US/09999025
; Publication No. US20020183497A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,025
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-999-025-10
Query Match      89.8%; Score 543; DB 9; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 4
US-09-999-040-10
; Sequence 10, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-999-040-10
Query Match      89.8%; Score 543; DB 9; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 4
US-09-999-040-10
; Sequence 1, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
```

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; LOCATION: 1..115
US-09-999-040-10
Query Match      89.8%; Score 543; DB 9; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 5
US-09-999-040-10
; Sequence 10, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-999-040-10
Query Match      89.8%; Score 543; DB 9; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHWVKQNPQQRLEWIGYFSPGNDPFKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 6
US-09-998-817-1
; Sequence 1, Application US/09998817
; Publication No. US20030004318A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal
```

```
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE:
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/998,817
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-998-817-1

Query Match      89.8%; Score 543; DB 10; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWVKQNPQORLEWIGYSPGNDDPKY 60
Db 1 QVQLQQSDAELVKPGASVKISKASGYTFTDHAHWVKQNPQORLEWIGYSPGNDDPKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVTSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVTSS 115

Query Match      89.8%; Score 543; DB 10; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVTSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVTSS 115

RESULT 7
US-09-998-817-10
; Sequence 10, Application US/09998817
; Publication No. US20030004318A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/998,817
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-998-817-10

Query Match      89.8%; Score 543; DB 10; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWVKQNPQORLEWIGYSPGNDDPKY 60
Db 1 QVQLQQSDAELVKPGASVKISKASGYTFTDHAHWVKQNPQORLEWIGYSPGNDDPKY 60

Qy 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTSLTVTSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVTSS 115

RESULT 9
US-09-999-021-1
; Sequence 10, Application US/09999021
; Publication No. US20030013854A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
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; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-999-021-10

Query Match      89.8%; Score 543; DB 10; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 10
US-10-040-997-1
; Sequence 1, Application US/10040997
; Publication No. US20030013856A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/040,997
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-10-040-997-1

Query Match      89.8%; Score 543; DB 14; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 11
US-10-040-997-10
; Sequence 10, Application US/10040997
; Publication No. US20030013856A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/040,997
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-10-040-997-1

Query Match      89.8%; Score 543; DB 14; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.3e-42;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYFTTDAIHHWKQNPQORLEWIGYFSPGNDDPKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTRSLNMYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGTSLTVSS 115

RESULT 12
US-10-255-478-74
; Sequence 74, Application US/10255478
; Publication No. US20030165498A1
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padlan, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/10/255,478
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/08/961,309
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 08/261,354
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: US 07/964,536
; PRIOR FILING DATE: 1992-10-20
; PRIOR APPLICATION NUMBER: US 07/510,697
; PRIOR FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 74
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-10-255-478-74
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/ APPLICATION NUMBER: US/09/956,087
/ FILING DATE: 20-Sep-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/069,821
/ FILING DATE: 1998-04-30
/ APPLICATION NUMBER: US 60/063,074
/ FILING DATE: 27-OCT-1997
/ APPLICATION NUMBER: US 60/050,472
/ FILING DATE: 23-JUN-1997
/ APPLICATION NUMBER: US 60/044,449
/ FILING DATE: 30-APR-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KIM, JUDITH U.
/ REGISTRATION NUMBER: 40,679
/ REFERENCE/DOCKET NUMBER: 0977.2280003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)371-2600
/ TELEFAX: (202)371-2540
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 249 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-956-087-2

Query Match 89.1%; Score 540; DB 9; Length 249;
Best Local Similarity 88.7%; Pred. No. 5.6e-42;
Matches 102; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSGNDDFKY 60
DB 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSGNDDFKY 191
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYVYFCTRSINMAYWGQGLTVTS 115
DB 192 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSINMAYWGQGLTVTSN 246

RESULT 16
US-09-791-578-6
/ Sequence 6, Application US/09791578
/ Patent No. US20020061307A1
/ GENERAL INFORMATION:
/ APPLICANT: WHITLOW, MARC
/ SHORR, ROBERT G.L.
/ FILPULA, DAVID R.
/ LEE, LIHSYNG S.
/ TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
/ POLYPEPTIDES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
/ STREET: 1100 NEW YORK AVENUE, SUITE 600
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/791,578
/ FILING DATE: 26-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/069,842
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 60/050,472

/ FILING DATE: 23-JUN-1997
/ APPLICATION NUMBER: US 60/063,074
/ FILING DATE: 27-OCT-1997
/ APPLICATION NUMBER: US 60/067,341
/ FILING DATE: 02-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: JORGE A. GOLDSTEIN
/ REGISTRATION NUMBER: 29,021
/ REFERENCE/DOCKET NUMBER: 0977.1840002
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 241 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-791-578-6

Query Match 89.1%; Score 539; DB 9; Length 241;
Best Local Similarity 89.5%; Pred. No. 6.7e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSGNDDFKY 60
DB 128 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYFSGNDDFKY 187
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYVYFCTRSINMAYWGQGLTVTS 114
DB 188 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSINMAYWGQGLTVTS 241

RESULT 17
US-09-791-540-6
/ Sequence 6, Application US/09791540
/ Patent No. US20020098192A1
/ GENERAL INFORMATION:
/ APPLICANT: WHITLOW, MARC
/ SHORR, ROBERT G.L.
/ FILPULA, DAVID R.
/ LEE, LIHSYNG S.
/ TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
/ POLYPEPTIDES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
/ STREET: 1100 NEW YORK AVENUE, SUITE 600
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/791,540
/ FILING DATE: 26-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/069,842
/ FILING DATE: 1998-04-30
/ APPLICATION NUMBER: US 60/050,472
/ FILING DATE: 23-JUN-1997
/ APPLICATION NUMBER: US 60/063,074
/ FILING DATE: 27-OCT-1997
/ APPLICATION NUMBER: US 60/067,341
/ FILING DATE: 02-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: JORGE A. GOLDSTEIN

```

;
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-791-540-6

Query Match      89.1%; Score 539; DB 9; Length 241;
Best Local Similarity 89.5%; Pred. No. 6.7e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0

QY      1 QVOLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNPQGLRWIGYFSPGNDDPKY 60
DB      128 QVQLQQSDAEIVKPGASVKISCKASGYTFDTHAIHWKQNPQGLRWIGYFSPGNDDPKY 187

QY      61 NERFKGKATLTADTASTAYVELSLRSEDPAVYFCTRSLNMYWGQGTTLVTS 114
DB      188 NERFKGKATLTADKSSSTAYVQLNSLTSSESAVYFCTRSLNMYWGQGTSTVTS 241

RESULT 18
US-10-915-069-6
; Sequence 6, Application US/10915069
; Publication No. US2005008650A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILFULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/915,069
; FILING DATE: 10-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,540
; FILING DATE: 26-Feb-2001
; APPLICATION NUMBER: 09/069,842
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

```



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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-909-948-6

Query Match      89.1%; Score 539; DB 17; Length 241;
Best Local Similarity 89.5%; Pred. No. 6.7e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 60
DB 128 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 187

QY 61 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 114
DB 188 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 241

RESULT 20
US-09-791-578-4
; Sequence 4, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,578
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-791-578-4

Query Match      89.1%; Score 539; DB 9; Length 257;
Best Local Similarity 89.5%; Pred. No. 7.1e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 60
DB 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 191

QY 61 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 114
DB 188 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 245

RESULT 21
US-09-791-540-4
; Sequence 4, Application US/09791540
; Patent No. US20020098192A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,540
; FILING DATE: 26-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/069,842
; FILING DATE: 1998-04-30
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-791-540-4

Query Match      89.1%; Score 539; DB 9; Length 257;
Best Local Similarity 89.5%; Pred. No. 7.1e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 60
DB 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLRWIGYFSPGNDDFKY 191

QY 61 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 114
DB 188 NERFKGKATLTADTSASTAYVELLSRSEDYAVYFCTRSINMAYWGQGLTVTVS 245
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Db 192 NERFKGATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNNAYWGQGTSTVTS 245

RESULT 22

US-09-983-580-2

Sequence 2, Application US/09983580

Patent No. US20020151061A1

GENERAL INFORMATION:

APPLICANT: Wang, Maoliang

APPLICANT: Filpula, David R.

APPLICANT: Whitlow, Marc D.

TITLE OF INVENTION: No. US20020151061A1el Method for Targeted Delivery of Nucleic Acid

FILE REFERENCE: 0977.2300002

CURRENT APPLICATION NUMBER: US/09/983,580

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: 09/420,592

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/104,949

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 257

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFv

US-09-983-580-2

Query Match 89.1%; Score 539; DB 9; Length 257;

Best Local Similarity 89.5%; Pred. No. 7,1e-42;

Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 60

Db 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 191

Qy 61 NERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLNNAYWGQGTSTVTS 114

Db 192 NERFKGATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNNAYWGQGTSTVTS 245

RESULT 23

US-09-985-442-2

Sequence 2, Application US/09985442

Patent No. US20020156248A1

GENERAL INFORMATION:

APPLICANT: Filpula, David R.

APPLICANT: Wang, Maoliang

APPLICANT: Whitlow, Marc D.

TITLE OF INVENTION: No. US20020156248A1el Method for Targeted Delivery of Nucleic Acid

FILE REFERENCE: 0977.2300003

CURRENT APPLICATION NUMBER: US/09/985,442

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: 09/420,592

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/104,949

PRIOR FILING DATE: 1998-10-20

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 257

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: CC49/218 sFv

US-09-985-442-2

Query Match 89.1%; Score 539; DB 9; Length 257;

Best Local Similarity 89.5%; Pred. No. 7,1e-42;

Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 60

Db 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 191

Qy 61 NERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLNNAYWGQGTSTVTS 114

Db 192 NERFKGATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNNAYWGQGTSTVTS 245

RESULT 24

US-10-915-069-4

Sequence 4, Application US/10915069

Publication No. US20050008650A1

GENERAL INFORMATION:

APPLICANT: WHITLOW, MARC

APPLICANT: FILPULA, DAVID R.

APPLICANT: SHORR, ROBERT G.L.

LEE, LIHSYNG S.

TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN POLYPEPTIDES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/915,069

FILING DATE: 10-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/791,540

FILING DATE: 26-Feb-2001

APPLICATION NUMBER: 09/069,842

FILING DATE: 1998-04-30

APPLICATION NUMBER: US 60/050,472

FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-OCT-1997

APPLICATION NUMBER: US 60/067,341

FILING DATE: 02-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: JORGE A. GOLDSTEIN

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0977.1840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-915-069-4

Query Match 89.1%; Score 539; DB 17; Length 257;

Best Local Similarity 89.5%; Pred. No. 7,1e-42;

Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 60

Db 132 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNPQGLEWIGYFSPGNDDFKY 191

Qy 61 NERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLNNAYWGQGTSTVTS 114

DB 192 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNWAYWGQGTSTVTS 245

RESULT 25

US-10-909-948-4
; Sequence 4, Application US/10909948
; Publication NO. US20050048064A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; SHORR, ROBERT G.L.
; FILPULA, DAVID R.
; LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
; POLYPEPTIDES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/909,948
; FILING DATE: 02-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/791,578
; FILING DATE: 26-Feb-2001
; APPLICATION NUMBER: 09/069,842
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/050,472
; FILING DATE: 23-JUN-1997
; APPLICATION NUMBER: US 60/063,074
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: US 60/067,341
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.1840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-909-948-4

Query Match 89.1%; Score 539; DB 17; Length 257;
Best Local Similarity 89.5%; Pred. No. 7.1e-42;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDAIHVKONPGORLEWIGYFSPGNDDFKY 60
DB 132 QVQLQSDRELVKPGASVKISKASGYTFTDAIHVKONPEGLEWIGYFSPGNDDFKY 191
QY 61 NERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRSLNWAYWGQGTSTVTS 114
DB 192 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNWAYWGQGTSTVTS 245

Search completed: July 25, 2005, 08:22:38
Job time : 107.961 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	605	100.0	115	4	US-08-961-309-76	Sequence 76, Appl
2	605	100.0	115	4	US-09-830-748B-14	Sequence 14, Appl
3	543	89.8	115	2	US-08-819-033-2	Sequence 2, Appl
4	543	89.8	115	3	US-09-025-203-1	Sequence 1, Appl
5	543	89.8	115	3	US-09-025-203-10	Sequence 10, Appl
6	543	89.8	115	4	US-08-961-309-74	Sequence 74, Appl
7	543	89.8	115	4	US-09-999-021-1	Sequence 1, Appl
8	543	89.8	115	4	US-09-999-021-10	Sequence 10, Appl
9	543	89.8	115	4	US-09-999-025-1	Sequence 1, Appl
10	543	89.8	115	4	US-09-999-025-10	Sequence 10, Appl
11	543	89.8	115	4	US-10-040-997-1	Sequence 1, Appl
12	543	89.8	115	4	US-10-040-997-10	Sequence 10, Appl
13	543	89.8	115	4	US-09-999-040-1	Sequence 1, Appl
14	543	89.8	115	4	US-09-999-040-10	Sequence 10, Appl
15	543	89.8	115	4	US-09-998-817-1	Sequence 1, Appl
16	543	89.8	115	4	US-09-998-817-10	Sequence 10, Appl
17	543	89.8	134	2	US-08-822-028-4	Sequence 4, Appl
18	543	89.8	134	2	US-08-822-028-29	Sequence 29, Appl
19	543	89.8	134	3	US-08-479-285-4	Sequence 4, Appl
20	543	89.8	134	3	US-08-479-285-29	Sequence 29, Appl
21	543	89.8	134	4	US-09-503-653A-4	Sequence 4, Appl
22	543	89.8	134	4	US-09-503-653A-29	Sequence 29, Appl
23	543	89.8	483	2	US-08-392-338A-19	Sequence 19, Appl
24	543	89.8	483	3	US-09-166-750-19	Sequence 19, Appl
25	543	89.8	483	3	US-09-166-093-19	Sequence 19, Appl
26	543	89.8	483	3	US-09-172-019-19	Sequence 19, Appl
27	543	89.8	483	3	US-09-166-094-19	Sequence 19, Appl

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,033
FILING DATE: 17-MAR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/417,855
FILING DATE: 07-APRIL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BUGAISKY, LAWRENCE B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0977.2220001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-819-033-2

Query Match 89.8%; Score 543; DB 2; Length 115;
Best Local Similarity 89.8%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
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DB 1 QVQLQSDAELVKPGASVKISCKASGYTFTDTHAIHWKQNPQGLRWIGVYFSPGNDDFKY 60
QY 61 NERFKGKATLTADTASATAYVELSLRSSEDTAVYFCTRSLNLMAYWQGGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNLMAYWQGGLTVTVSS 115

RESULT 4
US-09-025-203-1
Sequence 1, Application US/09025203
Patent No. 6348581
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/025,203
CURRENT FILING DATE: 1998-02-18
EARLIER APPLICATION NUMBER: PCT US97/19641
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 1
LENGTH: 115
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: Murine CC49 VH
LOCATION: 1..115
US-09-025-203-1

Query Match 89.8%; Score 543; DB 3; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGLRWIGVYFSPGNDDFKY 60
DB 1 QVQLQSDAELVKPGASVKISCKASGYTFTDTHAIHWKQNPQGLRWIGVYFSPGNDDFKY 60

QY 61 NERFKGKATLTADTASATAYVELSLRSSEDTAVYFCTRSLNLMAYWQGGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNLMAYWQGGLTVTVSS 115

RESULT 5

US-09-025-203-10
Sequence 10, Application US/09025203
Patent No. 6348581
GENERAL INFORMATION:
APPLICANT: Anderson, W.H. Kerr
APPLICANT: Tempest, Philip R.
APPLICANT: Carr, Frank J.
APPLICANT: Harris, William J.
APPLICANT: Armour, Kathryn
TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/025,203
CURRENT FILING DATE: 1998-02-18
EARLIER APPLICATION NUMBER: PCT US97/19641
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 10
LENGTH: 115
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: Murine CC49 VH
LOCATION: 1..115
US-09-025-203-10

Query Match 89.8%; Score 543; DB 3; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVVKPGASVKISCKASGYTFTDTHAIHWKQNPQGLRWIGVYFSPGNDDFKY 60
DB 1 QVQLQSDAELVKPGASVKISCKASGYTFTDTHAIHWKQNPQGLRWIGVYFSPGNDDFKY 60
QY 61 NERFKGKATLTADTASATAYVELSLRSSEDTAVYFCTRSLNLMAYWQGGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNLMAYWQGGLTVTVSS 115

RESULT 6

US-08-961-309-74
Sequence 74, Application US/08961309
Patent No. 6495137
GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.
APPLICANT: Johnson, Kimberly S.
APPLICANT: Schlom, Jeffrey
APPLICANT: Kashmiri, Syed V.S.
APPLICANT: Shu, Liming
APPLICANT: Padlan, Eduardo A.
TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
FILE REFERENCE: 37777E
CURRENT APPLICATION NUMBER: US/08/961,309
CURRENT FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: US 60/030,173
EARLIER FILING DATE: 1996-10-31
EARLIER APPLICATION NUMBER: US 08/261,354
EARLIER FILING DATE: 1994-06-16
EARLIER APPLICATION NUMBER: US 07/964,536
EARLIER FILING DATE: 1992-10-20
EARLIER APPLICATION NUMBER: US 07/510,697
EARLIER FILING DATE: 1990-07-17


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; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-999-040-1

Query Match      89.8%; Score 543; DB 4; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQQSDAEILVKPGASVKISKASGYTFTDHAHHWKQNPQEGLEWIGYFSPGNDDPKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTSLNWAYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNWAYWGQGTSLTVSS 115

RESULT 14
US-09-999-040-1
; Sequence 10, Application US/09999040
; Patent No. 6753152
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,817
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-998-817-1

Query Match      89.8%; Score 543; DB 4; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNPQORLEWIGYFSPGNDDPKY 60
Db 1 QVQLQQSDAEILVKPGASVKISKASGYTFTDHAHHWKQNPQEGLEWIGYFSPGNDDPKY 60

Qy 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTSLNWAYWGQGTSLTVSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNWAYWGQGTSLTVSS 115

RESULT 16
US-09-998-817-10
; Sequence 10, Application US/09998817
; Patent No. 6753420
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,817
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 1
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-998-817-1
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; CURRENT APPLICATION NUMBER: US/09/998,817
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 10
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VH
; LOCATION: 1..115
US-09-998-817-10

Query Match      89.8%; Score 543; DB 4; Length 115;
Best Local Similarity 89.6%; Pred. No. 1.8e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
DB      1 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
QY      61 NERFKGKATLTADTASATYAVVLSLRSDDTAVYFCTSLNMYWGQGTSLVTVSS 115
DB      61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNMYWGQGTSLVTVSS 115

RESULT 17
US-08-822-028-4
; Sequence 4, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-028-29

Query Match      89.8%; Score 543; DB 2; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
DB      1 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
QY      61 NERFKGKATLTADTASATYAVVLSLRSDDTAVYFCTSLNMYWGQGTSLVTVSS 115
DB      61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNMYWGQGTSLVTVSS 134

RESULT 18
US-08-822-028-29
; Sequence 29, Application US/08822028
; Patent No. 5993813
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHOLM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-028-29

Query Match      89.8%; Score 543; DB 2; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY      1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
DB      1 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQORLEWIGYSPGNDDFKY 60
QY      61 NERFKGKATLTADTASATYAVVLSLRSDDTAVYFCTSLNMYWGQGTSLVTVSS 115
DB      61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNMYWGQGTSLVTVSS 134
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Db 20 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWKQNPQGLEWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTLTVSS 115
Db 80 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNMYWGQGTSTVSS 134

RESULT 19
US-08-479-285-4
; Sequence 4, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,285
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040687
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-285-4

Query Match 89.8%; Score 543; DB 3; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQGLEWIGYFSPGNDDPKY 60
Db 20 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWKQNPQGLEWIGYFSPGNDDPKY 79

QY 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTLTVSS 115
Db 80 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNMYWGQGTSTVSS 134

RESULT 20
US-08-479-285-29
; Sequence 29, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: Probing Method for Identifying Antibodies
; FILE REFERENCE: 37075H-CIP1
; CURRENT APPLICATION NUMBER: US/09/503,653A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 08/040,687
; PRIOR FILING DATE: 1993-03-31
; APPLICANT: MEZES, PETER S
```

```
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,285
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040687
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37,075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-285-29

Query Match 89.8%; Score 543; DB 3; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQGLEWIGYFSPGNDDPKY 60
Db 20 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWKQNPQGLEWIGYFSPGNDDPKY 79

QY 61 NERFKGKATLTADTTSASTAYVELSLRSEDYAVYFCTRSLNMYWGQGTLTVSS 115
Db 80 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSLNMYWGQGTSTVSS 134

RESULT 21
US-09-503-653A-4
; Sequence 4, Application US/09503653A
; Patent No. 6641999
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
; APPLICANT: Gourlie, Brian B
; APPLICANT: Rixon, Mark W
; APPLICANT: Anderson, WH Kerr
; APPLICANT: Kaplan, Donald A
; APPLICANT: Schlom, Jeffrey
; TITLE OF INVENTION: Probing Method for Selected Antigens
; FILE REFERENCE: 37075H-CIP1
; CURRENT APPLICATION NUMBER: US/09/503,653A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 08/040,687
; PRIOR FILING DATE: 1993-03-31
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;; PRIOR APPLICATION NUMBER: US 07/424,362
;; PRIOR FILING DATE: 1989-10-19
;; PRIOR APPLICATION NUMBER: US 07/261,942
;; PRIOR FILING DATE: 1988-10-24
;; PRIOR APPLICATION NUMBER: US 07/259,943
;; PRIOR FILING DATE: 1988-10-19
;; NUMBER OF SEQ ID NOS: 74
;; SOFTWARE: MICROSOFT Word 97 SR-2
;; SEQ ID NO 4
;; LENGTH: 134
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: -19..-1
;; NAME/KEY: CHAIN
;; LOCATION: 1..115
US-09-503-653A-4

Query Match 89.8%; Score 543; DB 4; Length 134;
Best Local Similarity 89.8%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 60
DB 20 QVQLQSDAELVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSINMAYWGQGLTVTVSS 134

RESULT 22
US-09-503-653A-29
; Sequence 29, Application US/09503653A
; Patent No. 6641999
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
; APPLICANT: Gourlie, Brian B
; APPLICANT: Rixon, Mark W
; APPLICANT: Anderson, WH Kerr
; APPLICANT: Kaplan, Donald A
; APPLICANT: Schlom, Jeffrey
; TITLE OF INVENTION: Probing Method for Identifying Antibodies
; FILE OF INVENTION: Specific for Selected Antigens
; FILE REFERENCE: 3707SH-CIP1
; CURRENT APPLICATION NUMBER: US/09/503,653A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 08/040,687
; PRIOR FILING DATE: 1993-03-31
; PRIOR APPLICATION NUMBER: US 07/424,362
; PRIOR FILING DATE: 1989-10-19
; PRIOR APPLICATION NUMBER: US 07/261,942
; PRIOR FILING DATE: 1988-10-24
; PRIOR APPLICATION NUMBER: US 07/259,943
; PRIOR FILING DATE: 1988-10-19
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: MICROSOFT Word 97 SR-2
; SEQ ID NO 29
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-653A-29

Query Match 89.8%; Score 543; DB 4; Length 134;
Best Local Similarity 89.8%; Pred. No. 2.2e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 60
DB 20 QVQLQSDAELVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWGQGLTVTVSS 115

Db 80 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSINMAYWGQGLTVTVSS 134

RESULT 23
US-08-392-338A-19
; Sequence 19, Application US/08392338A
; Patent No. 5869620
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James P.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,338A
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.0030007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-392-338A-19

Query Match 89.8%; Score 543; DB 2; Length 483;
Best Local Similarity 89.6%; Pred. No. 9.5e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 60
DB 128 QVQLQSDAELVKPGASVKISCKASGYTFTDHAHWKQNPQGLRWIGYFSPGNDDFKY 187

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTRSINMAYWGQGLTVTVSS 115
DB 188 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTRSINMAYWGQGLTVTVSS 242

RESULT 24
US-09-166-750-19
; Sequence 19, Application US/09166750
; Patent No. 6025165
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James P.

```

; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/166,750
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-166-750-19

Query Match      89.8%; Score 543; DB 3; Length 483;
Best Local Similarity 89.6%; Pred. No. 9.5e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYSPGNDDPKY 60
Db      128 QVQLQQSDAELVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYSPGNDDPKY 187

Qy      61 NERFKGKATLTADTASATAYVELSLRSEDVAVYFCTSLNNAYWGQGTSLTVSS 115
Db      188 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNNAYWGQGTSLTVSS 242

RESULT 25
US-09-166-093-19
; Sequence 19, Application US/09166093
; Patent No. 6027725
; GENERAL INFORMATION:
; APPLICANT: Whitlow, Marc
; APPLICANT: Wood, James F.
; APPLICANT: Hardman, Karl
; APPLICANT: Bird, Robert
; APPLICANT: Filpula, David
; APPLICANT: Rollence, Michelle
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 23

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/166,093
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/392,338
; FILING DATE: 22-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/989,846
; FILING DATE: 20-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,936
; FILING DATE: 25-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0977.003000B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 483 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-166-093-19

Query Match      89.8%; Score 543; DB 3; Length 483;
Best Local Similarity 89.6%; Pred. No. 9.5e-47;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy      1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYSPGNDDPKY 60
Db      128 QVQLQQSDAELVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYSPGNDDPKY 187

Qy      61 NERFKGKATLTADTASATAYVELSLRSEDVAVYFCTSLNNAYWGQGTSLTVSS 115
Db      188 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNNAYWGQGTSLTVSS 242

Search completed: July 25, 2005, 08:12:50
Job time : 32.131 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:32:04 ; Search time 122.031 Seconds
(without alignments)
364.478 Million cell updates/sec

Title: US-10-058-069-7_COPY=20_134
Perfect score: 605
Sequence: 1 QVQLVQSGAEVVKPGASVKI.....CTRSLNMAVWGQGLTVTVSS 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Genesecp20004s: *
1: Genesecp1980s: *
2: Genesecp1990s: *
3: Genesecp2000s: *
4: Genesecp2001s: *
5: Genesecp2002s: *
6: Genesecp2003s: *
7: Genesecp2003bs: *
8: Genesecp2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	100.0	115	3	Aay95244 Humanised
2	605	100.0	115	6	Adb17748 Humanised
3	605	100.0	115	7	Adg46868 Humanised
4	605	100.0	134	6	Adb17752 Humanised
5	605	100.0	134	7	Adg46873 Humanised
6	605	100.0	354	5	Aae27926 Human CH2
7	605	100.0	354	6	Abb28285 Antibody
8	543	89.8	115	2	Aay42261 Murine an
9	543	89.8	115	5	Aau78314 Murine CC
10	543	89.8	115	6	Abu09362 Murine mo
11	543	89.8	115	6	Abu09368 Heavy cha
12	543	89.8	115	6	Abu10137 Murine TA
13	543	89.8	115	6	Abu10137 Murine TA
14	543	89.8	115	6	Abu17746 Native CC
15	543	89.8	115	6	Abu62751 Murine CC
16	543	89.8	115	6	Abu62760 Murine mo
17	543	89.8	115	7	Aae39057 Murine CC
18	543	89.8	115	7	Adg46866 Murine CC
19	543	89.8	115	8	Adf71403 Mouse CC4
20	543	89.8	134	2	Aar04383 Colon Can
21	543	89.8	134	2	Aay50685 Human CC4
22	543	89.8	134	2	Aay57176 Amino aci
23	543	89.8	134	3	Aay57047 Amino aci
24	543	89.8	134	3	Aay90715 CC49 VH r
25	543	89.8	134	3	Aay90722 CC49 VH r

26	543	89.8	134	4	Aau02141	Aau02141 Mouse ant
27	543	89.8	134	4	Aau02134	Aau02134 Mouse car
28	543	89.8	134	7	Adk66841	Adk66841 Mouse CC4
29	543	89.8	134	7	Adk66816	Adk66816 Mouse CC4
30	543	89.8	262	4	Aab31421	Aab31421 Protein u
31	543	89.8	483	2	Aaw88099	Aaw88099 A protein
32	543	89.8	483	3	Aab07935	Aab07935 A divalen
33	543	89.8	483	3	Aay57254	Aay57254 Divalent
34	543	89.8	483	3	Aab27679	Aab27679 Bivalent
35	543	89.8	483	3	Aay80924	Aay80924 Bivalent
36	543	89.8	483	6	Abu61809	Abu61809 Divalent
37	543	89.8	486	2	Aar37649	Aar37649 Sequence
38	540	89.3	115	2	Aar56965	Aar56965 CC49 V-he
39	540	89.3	115	2	Aay97178	Aay97178 Monoclonal
40	540	89.3	115	2	Aay05760	Aay05760 Anti-TAG-
41	540	89.3	249	2	Aaw97888	Aaw97888 CC49/218
42	540	89.3	275	2	Aar49137	Aar49137 Sequence
43	540	89.3	285	2	Aar48638	Aar48638 Sequence
44	540	89.3	553	2	Aar56967	Aar56967 CC49 VL-L
45	540	89.3	553	2	Aar56966	Aar56966 CC49 VL-L
46	540	89.3	553	2	Aaw97181	Aaw97181 A multiva
47	540	89.3	553	2	Aaw97180	Aaw97180 A multiva
48	540	89.3	553	2	Aay05762	Aay05762 CC49 sing
49	540	89.3	553	2	Aay05763	Aay05763 CC49 sing
50	539	89.1	238	2	Aar55864	Aar55864 4-4-20 VL
51	539	89.1	238	2	Aaw95438	Aaw95438 Linked fu
52	539	89.1	238	2	Aaw88100	Aaw88100 Single ch
53	539	89.1	238	3	Aab07936	Aab07936 A single-
54	539	89.1	238	3	Aay57255	Aay57255 4-4-20 VL
55	539	89.1	238	3	Aab27680	Aab27680 Bivalent
56	539	89.1	238	3	Aay80925	Aay80925 Single ch
57	539	89.1	238	3	Aay54834	Aay54834 Antibody
58	539	89.1	238	6	Abu61810	Abu61810 Antigen b
59	539	89.1	240	2	Aaw88095	Aaw88095 Single-ch
60	539	89.1	240	3	Aab07931	Aab07931 A heterob
61	539	89.1	240	3	Aay57250	Aay57250 4-4-20 VL
62	539	89.1	240	3	Aab27675	Aab27675 Bivalent
63	539	89.1	240	3	Aay80920	Aay80920 Single ch
64	539	89.1	240	6	Abu61805	Abu61805 Antigen b
65	539	89.1	248	2	Aar97382	Aar97382 CC49 VL-P
66	539	89.1	257	2	Aaw81524	Aaw81524 Single ch
67	539	89.1	257	5	Aau75157	Aau75157 CC49/218
68	539	89.1	257	6	Abg73145	Abg73145 CC49/218
69	539	89.1	262	2	Aar97380	Aar97380 CC49/212
70	539	89.1	262	2	Aar97381	Aar97381 PLAP CC49
71	539	89.1	262	2	Aar97381	Aar97381 PLAP CC49
72	539	89.1	269	5	Aau75158	Aau75158 CC49/218
73	539	89.1	269	6	Abg73146	Abg73146 CC49/218
74	539	89.1	269	6	Abg73146	Abg73146 CC49/218
75	539	89.1	444	6	Abj39018	Abj39018 CC49 sing
76	537	88.8	134	2	Aar38312	Aar38312 Sequence
77	536	88.6	275	2	Aar49139	Aar49139 Sequence
78	536	88.6	280	2	Aar49138	Aar49138 Sequence
79	536	88.6	282	2	Aar48636	Aar48636 Sequence
80	536	88.6	282	2	Aar48635	Aar48635 Sequence
81	535	88.4	238	2	Aar37650	Aar37650 Single-ch
82	535	88.4	241	2	Aar37645	Aar37645 Multivale
83	534	88.3	134	6	Adb17719	Adb17719 Heavy cha
84	534	88.3	134	7	Adg46839	Adg46839 Mouse CC4
85	534	88.3	246	2	Aaw81523	Aaw81523 Single ch
86	534	88.3	251	2	Aar48632	Aar48632 Sequence
87	534	88.3	260	2	Aar38318	Aar38318 Sequence
88	534	88.3	260	2	Aay50691	Aay50691 Human SCF
89	534	88.3	260	2	Aay57182	Aay57182 Amino aci
90	534	88.3	260	6	Adb17736	Adb17736 SCFV1. 11
91	534	88.3	260	7	Adg46856	Adg46856 SCFV1 fus
92	533.5	88.2	274	2	Aay50692	Aay50692 Human Hum
93	533.5	88.2	274	2	Aay57183	Aay57183 Amino aci
94	533.5	88.2	274	6	Adb17738	Adb17738 Hum4 VL-C
95	533.5	88.2	274	7	Adg46858	Adg46858 Hum4VL-Li
96	533.5	88.2	284	2	Aay50694	Aay50694 plasmid p
97	533.5	88.2	284	2	Aay57185	Aay57185 Amino aci
98	533.5	88.2	284	6	Adb17742	Adb17742 pSC49FLAG

99 533.5 88.2 284 7 ADG46862 Hum4VL-li
100 530.5 87.7 284 2 AAR38321 Sequence

ALIGNMENTS

RESULT 1
AA95244
ID AA95244 standard; protein; 115 AA.
XX
AC AA95244;
XX
DT 12-SEP-2003 (revised)
DT 29-AUG-2000 (first entry)
XX
XX Humanised antibody HuCC49 heavy chain variable region.
XX
XX Humanised antibody; monoclonal antibody; CC49; HuCC49; CDR;
KW complementarity determining region; mouse; human; carcinoma;
KW colon cancer; tumor associated glycoprotein-72; TAG-72; tumour marker;
KW diagnosis; therapy.
XX
XX Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /note= "CDR1"
FT Region 50..67
FT /note= "CDR2"
FT Region 99..104
FT /note= "CDR3"
XX
XX WO200026394-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025552.
XX
XX 31-OCT-1998; 98US-0106534P.
XX 02-NOV-1998; 98US-0106757P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kashmiri SVS, Padlan EA, Schlom J;
XX WPI; 2000-365637/31.
XX
XX Chimeric variants of CC49 monoclonal antibodies useful for detecting and
PT treating cancers associated with the expression of the pancreaticoma tumor
PT -associated antigen TAG-72.
XX
XX Disclosure; Fig 4; 76pp; English.
XX
XX The present sequence is that of the heavy chain variable region (VH) of
CC HuCC49, a humanised monoclonal antibody (MAB) formed by grafting
CC hypervariable regions from murine MAB CC49 into VL and VH frameworks of
CC human MABs LEN and 21/28' CL, respectively, while retaining murine
CC framework residues required for integrity of the antigen combining site
CC structure. HuCC49 binds to the human pancreaticoma tumor associated
CC glycoprotein-72 (TAG-72), which is found on the surface of certain human
CC tumours. The invention is directed towards mouse-human chimeric variants
CC of CC49 MABs with minimal murine content, to methods of making such
CC variants, and their therapeutic application. The invention provides
CC complementarity determining region (CDR) variants of HuCC49 in which
CC fewer than all 6 CDRs of CC49 are present, and specificity determining
CC region (SDR) variants of HuCC49 in which only SDRs of at least 1 CDR from
CC CC49 are present. Particular variants of HuCC9 have either 1-CDR1 and/or
CC L-CDR2 from human MAB LEN. These variants have the same or 2-fold lower
CC affinity constant than HuCC49. Other variants additionally have
CC corresponding human residues at position 97 of L-CDR3, and positions 60,

CC 61, 62 and 64 of H-CDR2, or have residues 31, 32 and 34 of H-CDR1 from a
CC non-human anti-TAG-12 antibody. The variants are used in claimed methods
CC of treating cancer and for detecting cancer cells that express TAG-72.
XX (Updated on 12-SEP-2003 to standardise OS field)
XX Sequence 115 AA;
XX
XX Query Match 100.0%; Score 605; DB 3; Length 115;
XX Best Local Similarity 100.0%; Pred. No. 5.8e-47;
XX Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQRLIEWIGYFSPGNDDFKY 60
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQRLIEWIGYFSPGNDDFKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSLNMYWGQGLTVTVSS 115
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSLNMYWGQGLTVTVSS 115
RESULT 2
ADBI7748
ID ADBI7748 standard; protein; 115 AA.
XX
XX ADBI7748;
XX
XX 20-NOV-2003 (first entry)
XX
XX Humanised CC49 heavy chain variable region fragment.
XX anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAWA; accelerated whole body clearance; human; mouse.
XX
XX Mus musculus.
OS Homo sapiens.
XX
XX US6495137-B1.
XX
XX 17-DEC-2002.
XX
XX 30-OCT-1997; 97US-00961309.
XX
XX 19-APR-1990; 90US-00510697.
XX 20-OCT-1992; 92US-00964536.
XX 16-JUN-1994; 94US-00261354.
XX 31-OCT-1996; 96US-0030173P.
XX
XX (DOWC) DOW CHEM CO.
XX
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
XX Padlan EA;
XX
XX WPI; 2003-615251/58.
XX
XX New composite and humanized anti-tumor-associated glycoprotein-72
PT monoclonal antibody useful for detecting or treating cancer.
XX
XX Claim 3; Fig 32B; 130pp; English.
XX
XX The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (TAG-72) antibody or its fragment comprising a
CC complementarity determining region (CDR)-grafted light chain having light
CC chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
CC IV kappa light chain. The composition is suitable for the treatment and
CC detection of cancer. The novel antibody has the ability to bind
CC specifically to malignant cells and does not bind to normal cells. It
CC greatly minimises or eliminates harmful hypersensitivity anti-mouse
CC antibody (HAWA) responses. The relatively small size and human character
CC of the composite Hum4V-L, V-H single chain antibodies accelerate whole
CC body clearance, thus reducing the waiting period after injection before
CC surgery is initiated. The present sequence represents the amino acid

CC sequence of the humanised CC49 heavy chain variable region fragment.
XX Sequence 115 AA;
SQ

Query Match 100.0%; Score 605; DB 6; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.8e-47; Indels 0; Gaps 0;
Matches 115; Conservative 0; Mismatches 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDPKY 60
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDPKY 60

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNWAYVGGTTLTVSS 115
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNWAYVGGTTLTVSS 115

RESULT 3
ADG46868
ID ADG46868 standard; protein; 115 AA.
XX
AC ADG46868;
DT
DT 11-MAR-2004 (first entry)
XX
DE Humanised CC49 VH protein fragment with 21/28'CL VH framework regions.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; mouse; human; chimeric.
XX
OS Chimeric.
OS Unidentified.
OS Mus musculus.
OS Homo sapiens.
XX

Key Location/Qualifiers
FT Region 1..30
FT /note= "Human LEN heavy chain variable region FR1"
FT Region 31..35
FT /note= "Murine CC49 heavy chain variable region CDR1"
FT Region 36..49
FT /note= "Human LEN heavy chain variable region FR2"
FT Region 50..66
FT /note= "Murine CC49 heavy chain variable region CDR2"
FT Region 67..98
FT /note= "Human LEN heavy chain variable region FR3"
FT Region 99..104
FT /note= "Murine CC49 heavy chain variable region CDR3"
FT Region 105..115
FT /note= "Human LEN heavy chain variable region FR4"
XX
PN US2003165498-A1.
XX
XX
PD 04-SEP-2003.
XX
PF 25-SEP-2002; 2002US-00255478.
XX
XX 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97US-00961309.
XX
PA (MEZE/) MEZES P S.
PA (RICH/) RICHARD R A.
PA (JOHN/) JOHNSON K S.
PA (SCHL/) SCHLOM J.
PA (KASH/) KASHMIRI S V S.
PA (SHUL/) SHU L.
PA (PADL/) PADLAN E A.
XX

PI Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
DR WPI; 2003-898033/82.
XX
PT New humanized or composite anti-TAG-72 monoclonal antibody with subgroup
PT IV kappa light chain framework regions, useful in the fields of
PT immunology and genetic engineering, particularly for detecting and/or
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 76; 133pp; English.
XX
CC The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody
CC comprises a complementarity determining region (CDR)-grafted light chain
CC having non-human CDRs grafted to a human subgroup IV kappa light chain.
CC The invention is useful in gene-therapy. The methods and compositions of
CC the present invention are useful in the fields of immunology and genetic
CC engineering, particularly for detecting and/or treating cancer. The
CC present sequence is humanised CC49 VH protein fragment with 21/28'CL VH
CC framework regions used in the exemplification of the invention.
XX
SQ Sequence 115 AA;
XX

Query Match 100.0%; Score 605; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.8e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDPKY 60
DB 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNPQORLEWIGYFSPGNDPKY 60

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNWAYVGGTTLTVSS 115
DB 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNWAYVGGTTLTVSS 115

RESULT 4
ADB17752
ID ADB17752 standard; protein; 134 AA.
XX
AC ADB17752;
XX
DT 20-NOV-2003 (first entry)
XX
DE Humanised CC49 heavy chain variable region.
XX
KW anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAMA; accelerated whole body clearance; human; mouse.
XX
OS Mus musculus.
OS Homo sapiens.
XX
PN US6495137-B1.
XX
PD 17-DEC-2002.
XX
PF 30-OCT-1997; 97US-00961309.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
XX
PA (DOWC) DOW CHEM CO.
XX
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-615251/58.
DR N-PSDB; ADB17750.
DR

```
XX PT New composite and humanized anti-tumor-associated glycoprotein-72
XX PT monoclonal antibody useful for detecting or treating cancer.
XX PS Disclosure; Col 113-114; 130pp; English.
XX
CC CC The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (TAG-72) antibody or its fragment comprising a
CC complementarity determining region (CDR)-grafted light chain having light
CC chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
CC IV kappa light chain. The composition is suitable for the treatment and
CC detection of cancer. The novel antibody has the ability to bind
CC specifically to malignant cells and does not bind to normal cells. It
CC greatly minimises or eliminates harmful hypersensitivity anti-mouse
CC antibody (HAMA) responses. The relatively small size and human character
CC of the composite Hum4V-L, V-H single chain antibodies accelerate whole
CC body clearance, thus reducing the waiting period after injection before
CC surgery is initiated. The present sequence represents the amino acid
CC sequence of the humanised CC49 heavy chain variable region.
XX
SQ Sequence 134 AA;
Query Match 100.0%; Score 605; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.8e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWKQNPQORLEWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSS 134
RESULT 5
ADG46873
ID ADG46873 standard; protein; 134 AA.
XX
AC ADG46873;
XX
DT 11-MAR-2004 (first entry)
XX
DE Humanised CC49 VH protein with 21/28'CL VH framework regions.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; mouse; human; fusion protein.
XX
OS Chimeric.
OS Unidentified.
OS Mus musculus.
OS Homo sapiens.
XX
XX US2003165498-A1.
XX
PD 04-SEP-2003.
XX
XX 25-SEP-2002; 2002US-00255478.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97US-00961309.
XX
XX (MEZE/) MEZES P S.
PA (RICH/) RICHARD R A.
PA (JOHN/) JOHNSON K S.
PA (SCHL/) SCHLUM J.
PA (KASH/) KASHMIRI S V S.
PA (SHUL/) SHU L.
XX
```

```
(PADL/) PADLAN E A.
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-898033/82.
XX N-PSDB; ADG46870.
XX
XX New humanized or composite anti-TAG-72 monoclonal antibody with subgroup
XX IV kappa light chain framework regions, useful in the fields of
XX immunology and genetic engineering, particularly for detecting and/or
XX treating cancer.
XX
XX Disclosure; SEQ ID NO 81; 133pp; English.
XX
XX The invention relates to a humanised or composite anti-tumour-associated
XX glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody
XX comprises a complementarity determining region (CDR)-grafted light chain
XX having non-human CDRs grafted to a human subgroup IV kappa light chain.
XX The invention is useful in gene-therapy. The methods and compositions of
XX the present invention are useful in the fields of immunology and genetic
XX engineering, particularly for detecting and/or treating cancer. The
XX present sequence is humanised CC49 VH protein with 21/28'CL VH framework
XX regions used in the exemplification of the invention.
XX
SQ Sequence 134 AA;
Query Match 100.0%; Score 605; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 6.8e-47;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHWKQNPQORLEWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRLNWAYWGQGLTVTVSS 134
RESULT 6
AAE27926
ID AAE27926 standard; protein; 354 AA.
XX
AC AAE27926;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human CH2 domain deleted CC49 antibody heavy chain protein.
XX
KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS Homo sapiens.
XX
XX WO200260955-A2.
XX
XX 08-AUG-2002.
XX
XX 29-JAN-2002; 2002WO-US002373.
XX
XX 29-JAN-2001; 2001US-0264318P.
XX 16-NOV-2001; 2001US-0331481P.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Braslawsky GR, Hanna N, Chinn P;
XX
XX WPI; 2002-698547/75.
XX N-PSDB; AAD45755.
XX
XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
XX
```

PT -72, or C2B8 antibody reactive with CD20, useful for treating
PT myelosuppressed patient suffering from a neoplastic disorder.

PS Example 2; Fig 4A; 74pp; English.

XX The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC deleted sequence in which CH2 domain has been deleted and are reactive
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC with CD20 and comprise a heavy chain having a sequence of a derived
CC domain deleted C2B8 construct where the CH2 domain has been deleted.
CC Sequences of the invention are useful for imaging a neoplasm. They are
CC also useful for treating myelosuppressed patients suffering from
CC neoplastic disorder such as haematologic neoplasm, preferably non-
CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC neoplastic disorder, colon cancer and haematologic malignancy. They are
CC useful for reducing tumour size, inhibiting tumour growth and/or
CC prolonging the survival time of tumour-bearing animals and for treating
CC tumours. The present sequence is human CH2 domain deleted CC49 antibody
CC heavy chain protein. This sequence is used in the exemplification of the
XX invention

SQ Sequence 354 AA;

Query Match 100.0%; Score 605; DB 5; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQRLIEWIGYFSPGNDPKY 60
DB 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQRLIEWIGYFSPGNDPKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 134

RESULT 7

ABB82835
ID ABB82835 standard; protein; 354 AA.

XX
AC ABB82835;

XX 31-MAR-2003 (first entry)

DE Antibody huCC49 CH2 domain deleted heavy chain.

XX CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antiinflammatory.

OS Homo sapiens.

PN WO200296948-A2.

XX 05-DEC-2002.

PF 29-JAN-2002; 2002WO-US002374.

XX 29-JAN-2001; 2001US-0264318P.

PR 16-NOV-2001; 2001US-0331481P.

XX 21-DEC-2001; 2001US-0341858P.

PA (IDEC-) IDEC PHARM CORP.

XX Braelawsky GR, Harna N, Chinn P, Hariharan K;

XX WPI; 2003-140446/13.

DR N-PSDB; AB224019.

PT Novel dimeric antibody useful for treating immune disorder and neoplastic

PT disorder, has several non-covalently associated monomeric subunits.

PS Example 1; Fig 4A; 78pp; English.

XX The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see AB224017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody huCC49 CH2 domain deleted heavy chain

XX Sequence 354 AA;

Query Match 100.0%; Score 605; DB 6; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.9e-46;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQRLIEWIGYFSPGNDPKY 60
DB 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNPQRLIEWIGYFSPGNDPKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 115

DB 80 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 134

RESULT 8

AAV42261

ID AAV42261 standard; protein; 115 AA.

XX
AC AAV42261;

XX 01-DEC-1999 (first entry)

DE Murine anti-TAG-72 monoclonal antibody CC49 VH region.

XX Tumour-associated glycoprotein; TAG-72; carcinoma; cancer; tumour;
KW antibody; therapy; immunogenic; humanise.

XX Mus sp.

XX WO9943816-A1.

XX 02-SEP-1999.

XX 25-FEB-1998; 98WO-US003679.

XX 25-FEB-1998; 98WO-US003679.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;

XX WPI; 1999-540593/45.

XX New humanized murine antibody specific for TAG-72 antigen, for treatment
PT and diagnosis of cancer.

XX Example; Fig 1; 75pp; English.

XX This sequence represents murine monoclonal antibody CC49 heavy chain
CC variable region (VH). CC49 binds TAG-72 (tumour-associated glycoprotein),
CC a human pancreatic carcinoma antigen expressed by various human tumour cells.
CC CC49 could be used as an anticancer agent; however, as it is from a

foreign species, it may cause a neutralising antibody response in the patient. In addition, its constant domains are murine and it may not exhibit human effector functions. To overcome these potential problems, humanised CC49 derivative antibodies were produced. These were produced by obtaining the CC49 heavy and light chain variable sequences, identifying the complementarity determining regions (CDRs) and grafting the CDR-encoding DNA sequences onto human antibody framework DNA sequences. Such humanised antibodies can be used in cancer therapy. The antibodies can be used to treat or prevent TAG-72-expressing cancers (e.g. of breast, ovary, prostate or colon) and to detect TAG-72-expressing cells, either in vitro or in vivo (particularly by tumour imaging to identify tumours and metastases before surgery), for diagnosis or prognosis. As the humanised antibodies are not significantly immunogenic, (i.e. they do not induce a human anti-murine antibody or allergic response, or non-specific cytotoxicity) they can be administered repeatedly. They retain specificity for TAG-72, and have improved clearance (allowing efficient targeting) and metabolic properties

Sequence 115 AA;
Query Match 89.8%; Score 543; DB 2; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 1 QVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
Db 1 QVQLQQSDAELVKPGASVKISCKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
Qy 61 NERFKGKATLTADTSASTAYVELSLRSDEDTAVYFCTRLSLNMAWYGQGTTLVTSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRLSLNMAWYGQGTSTVTSS 115

RESULT 9
AAU78314
ID AAU78314 standard; protein; 115 AA.
XX AAU78314;
AC AAU78314;
DT 05-JUN-2002 (first entry)
XX Murine CC49 heavy chain variable region (VH).
DE CC49; antibody; heavy chain variable region; humanised antibody;
XX tumour-associated glycoprotein-72; TAG-72; pancreatic cancer;
KW tumour imaging; VH.
XX Mus musculus.
OS US6348581-B1.
PN 19-FEB-2002.
PD 18-FEB-1998; 98US-00025203.
XX 31-OCT-1996; 96US-0030173P.
XX 30-OCT-1997; 97WO-US019641.
PR (DOWC) DOW CHEM CO.
PA Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2002-266545/31.
XX New humanized antibody which binds tumor-associated glycoprotein-72,
PT useful for diagnosis of cancer e.g. for tumor imaging and for treatment
PT of cancer.
XX Example 1; Fig 1; 40pp; English.

The invention describes a humanised antibody which specifically binds tumour-associated glycoprotein-72 (TAG-72), a human pancreatic carcinoma antigen expressed by human tumour cells. The antibody comprises a NSWMM-grafted

humanised heavy chain variable region (VH), and a REI-grafted humanised light chain variable region (VL), or its fragment which specifically binds TAG-72. A composition containing the antibody is useful for treatment of cancer, and for in vivo or in vitro detection of cancer e.g. for tumour imaging. This sequence represents the murine CC49 heavy chain variable region used in production of the TAG-72 binding humanised antibody of the invention

Sequence 115 AA;
Query Match 89.8%; Score 543; DB 5; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
Qy 1 QVQLVQSGAEVVKPGASVKISCKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
Db 1 QVQLQQSDAELVKPGASVKISCKASGYTFDTHAIHWVKQNPQORLEWIGYFSPGNDDFKY 60
Qy 61 NERFKGKATLTADTSASTAYVELSLRSDEDTAVYFCTRLSLNMAWYGQGTTLVTSS 115
Db 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRLSLNMAWYGQGTSTVTSS 115

RESULT 10
ABU09362
ID ABU09362 standard; protein; 115 AA.
XX ABU09362;
AC ABU09362;
DT 08-JUL-2003 (first entry)
XX Murine monoclonal antibody CC49 variable heavy chain (CC49MuVH).
DE Murine; mouse; humanised monoclonal antibody; TAG-72; colon cancer;
KW tumour-associated glycoprotein-72; immunodetection; tumour cell;
KW surgical excision; disease status; cytostatic; CC49MuVH;
KW CC49 variable heavy chain.

Mus sp.
XX US2003013856-A1.
PN 16-JAN-2003.
PD 31-OCT-2001; 2001US-00040997.
XX 31-OCT-1996; 96US-0030173P.
XX 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX (ANDE/) ANDERSON W H K.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-401607/38.

Novel humanized antibody derived from a murine antibody that specifically binds tumor-associated glycoprotein-72, useful for treating and detecting cancer.

Claim 2; Fig 1; 29pp; English.
The present invention relates to a novel humanised monoclonal antibody, and its fragments which specifically binds tumour-associated glycoprotein -72 (TAG-72), where the humanised monoclonal antibody is derived from a murine monoclonal antibody (e.g. CC49) that binds TAG-72. The humanised monoclonal antibody, and its fragments are useful for the treating and detection of TAG-72 cancers which express TAG-72 (e.g. colon cancer). The cancer is detected by the immunodetection of in vivo tumour cells, which

CC may be removed by surgical excision. The humanised monoclonal antibody of
 CC the invention is useful as a immunodiagnostic agent both in vivo and in
 CC vitro, and also for repeated monitoring of the disease status of a
 CC patient. The present sequence represents murine monoclonal antibody CC49
 CC variable heavy chain (CC49MuVH)

XX Sequence 115 AA;
 SQ Query Match 89.8%; Score 543; DB 6; Length 115;
 Best Local Similarity 89.6%; Pred. No. 2.3e-41;
 Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 QVQLVSGAEVVKPGASVKISKASGYTFTDHAHWKONPGQRLWIGVFPSPGNDDFKY 60
 DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWKONPQEGLEWIGVFPSPGNDDFKY 60
 QY 61 NERFKGKATLTADTSASTAYVELSLRSSEDTAVYFCTSLNMAWYMQGGLTVTVSS 115
 DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNMAWYMQGGLTVTVSS 115

RESULT 11
 ABU09368
 ID ABU09368 standard; protein; 115 AA.

XX AC ABU09368;
 XX DT 08-JUL-2003 (first entry)
 XX DE Heavy chain variable region of murine CC49.
 XX KW Murine; mouse; humanised monoclonal antibody; TAG-72; colon cancer;
 KW tumour-associated glycoprotein-72; immunodetection; tumour cell;
 KW surgical excision; disease status; cytostatic; CC49;
 KW heavy chain variable region.

XX OS Mus sp.
 XX US2003013856-A1.
 PD 16-JAN-2003.
 XX 31-OCT-2001; 2001US-00040997.
 XX 31-OCT-1996; 96US-0030173P.
 PR 30-OCT-1997; 97WO-US019641.
 PR 18-FEB-1998; 98US-00025203.

XX (ANDE/) ANDERSON W H K.
 PA (TEMP/) TEMPEST P R.
 PA (CARR/) CARR F J.
 PA (HARR/) HARRIS W J.
 PA (ARMO/) ARMOUR K.
 XX Anderson WHK, Tempest PR, Carr FU, Harris WJ, Armour K;
 PI WPI; 2003-401607/38.
 XX Novel humanized antibody derived from a murine antibody that specifically
 PT binds tumor-associated glycoprotein-72, useful for treating and detecting
 PT cancer.
 XX Claim 2; Fig 3; 29pp; English.

XX The present invention relates to a novel humanised monoclonal antibody,
 CC and its fragments which specifically binds tumour-associated glycoprotein
 CC -72 (TAG-72), where the humanised monoclonal antibody is derived from a
 CC murine monoclonal antibody (e.g. CC49) that binds TAG-72. The humanised
 CC monoclonal antibody, and its fragments are useful for the treating and
 CC detection of TAG-72 cancers which express TAG-72 (e.g. colon cancer). The
 CC cancer is detected by the immunodetection of in vivo tumour cells, which
 CC may be removed by surgical excision. The humanised monoclonal antibody of
 CC the invention is useful as a immunodiagnostic agent both in vivo and in

CC vitro, and also for repeated monitoring of the disease status of a
 CC patient. The present sequence represents the heavy chain variable region
 CC of murine CC49
 XX Sequence 115 AA;
 SQ Query Match 89.8%; Score 543; DB 6; Length 115;
 Best Local Similarity 89.6%; Pred. No. 2.3e-41;
 Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVVKPGASVKISKASGYTFTDHAHWKONPGQRLWIGVFPSPGNDDFKY 60
 DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWKONPQEGLEWIGVFPSPGNDDFKY 60
 QY 61 NERFKGKATLTADTSASTAYVELSLRSSEDTAVYFCTSLNMAWYMQGGLTVTVSS 115
 DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSDSAVYFCTSLNMAWYMQGGLTVTVSS 115

RESULT 12
 ABU10143
 ID ABU10143 standard; protein; 115 AA.

XX AC ABU10143;
 XX DT 11-AUG-2003 (first entry)
 XX DE Murine TAG-72 antibody CC49 heavy chain variable region.
 XX KW Mouse; tumour-associated glycoprotein 72; TAG-72; antibody; CC49; cancer;
 KW tumour; tumour imaging; serum clearance.

XX OS Mus sp.
 XX FH Key Location/Qualifiers
 FT Region 31.35
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT Region 50.66
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT Region 99.104
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"

US2003013854-A1.
 PD 16-JAN-2003.
 XX 31-OCT-2001; 2001US-00999021.
 XX 31-OCT-1996; 96US-0030173P.
 PR 30-OCT-1997; 97WO-US019641.
 PR 18-FEB-1998; 98US-00025203.

XX (ANDE/) ANDERSON W H K.
 PA (TEMP/) TEMPEST P R.
 PA (CARR/) CARR F J.
 PA (HARR/) HARRIS W J.
 PA (ARMO/) ARMOUR K.

XX Anderson WHK, Tempest PR, Carr FU, Harris WJ, Armour K;
 PI WPI; 2003-438920/41.

XX Novel humanized monoclonal antibody which specifically binds tumor-
 PT associated glycoprotein-72 useful for treating cancer and in vivo imaging
 PT of tumors or cancer cells expressing the tumor-associated glycoprotein-
 PT 72.

XX Disclosure; Fig 3; 29pp; English.

XX The invention relates to a humanised antibody (or its fragment) which

CC specifically binds tumour-associated glycoprotein 72 (TAG-72) (the
CC antibody or its fragment is derived from a murine antibody which
CC specifically binds TAG-72). The humanised antibody is useful for in vivo
CC treatment of cancer, by intravenously administering a radionuclide-
CC labelled antibody, detecting tumour cells using a radionuclide activity
CC probe, and removing the detected tumour cells by surgical excision. The
CC radionuclide is (125)I or (131)I. A composition containing the humanised
CC antibody is useful for in vivo treatment of a mammal having a TAG-72
CC expressing cancer. A composition containing the humanised antibody is
CC useful for in vitro immunodetection of TAG-72 expressing cancer cells,
CC where the antibody or its fragments of the composition are bound to a
CC solid support and also for in vivo tumour imaging. The humanised
CC antibodies have little or no reduced immunogenicity in humans over murine
CC and chimeric antibodies and have improved serum clearance and metabolic
CC properties. The antibodies can be used over prolonged time periods. The
CC present sequence represents the amino acid sequence of the murine TAG-72
CC antibody CC49 heavy chain variable region
XX
SQ Sequence 115 AA;

Query Match 89.8%; Score 543; DB 6; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 1 QVQLQSDAELVKPGASVKISKASGYFTDTHAIHWKQNPQGLEWIGYFSPGNDDPKY 60
QY 61 NERFKGKATLTADTASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGLTVTVSS 115

RESULT 13
ABU010137
ID ABU010137 standard; protein; 115 AA.
XX
AC ABU010137;
DT 11-AUG-2003 (first entry)
XX
DE Murine TAG-72 antibody CC49 heavy chain variable region.
XX
KW Mouse; tumour-associated glycoprotein 72; TAG-72; antibody; CC49; cancer;
KW tumour; tumour imaging; serum clearance.
XX
OS Mus sp.

Key Location/Qualifiers
FH Region 31..35
FT /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 99..104
FT /label= CDR3
FT /note= "Complementarity determining region 3"

US2003013854-A1.
XX
XX 16-JAN-2003.
XX
XX 31-OCT-2001; 2001US-00999021.
XX
XX 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX
XX (ANDE/) ANDERSON W H K.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.

(ARMO/) ARMOUR K.
XX
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-438920/41.
XX Novel humanized monoclonal antibody which specifically binds tumor-
XX associated glycoprotein-72 useful for treating cancer and in vivo imaging
XX of tumors or cancer cells expressing the tumor-associated glycoprotein-
XX 72.
XX Disclosure; Fig 1; 29pp; English.
XX The invention relates to a humanised antibody (or its fragment) which
XX specifically binds tumour-associated glycoprotein 72 (TAG-72) (the
XX antibody or its fragment is derived from a murine antibody which
XX specifically binds TAG-72). The humanised antibody is useful for in vivo
XX treatment of cancer, by intravenously administering a radionuclide-
XX labelled antibody, detecting tumour cells using a radionuclide activity
XX probe, and removing the detected tumour cells by surgical excision. The
XX radionuclide is (125)I or (131)I. A composition containing the humanised
XX antibody is useful for in vivo treatment of a mammal having a TAG-72
XX expressing cancer. A composition containing the humanised antibody is
XX useful for in vitro immunodetection of TAG-72 expressing cancer cells,
XX where the antibody or its fragments of the composition are bound to a
XX solid support and also for in vivo tumour imaging. The humanised
XX antibodies have little or no reduced immunogenicity in humans over murine
XX and chimeric antibodies and have improved serum clearance and metabolic
XX properties. The antibodies can be used over prolonged time periods. The
XX present sequence represents the amino acid sequence of the murine TAG-72
XX antibody CC49 heavy chain variable region
XX
SQ Sequence 115 AA;

Query Match 89.8%; Score 543; DB 6; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQORLEWIGYFSPGNDDPKY 60
DB 1 QVQLQSDAELVKPGASVKISKASGYFTDTHAIHWKQNPQGLEWIGYFSPGNDDPKY 60
QY 61 NERFKGKATLTADTASTAYVELSLRSEDYAVYFCTRSLNMYWGQGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGLTVTVSS 115

RESULT 14
ADBI7746
ID ADBI7746 standard; protein; 115 AA.
XX
XX ADBI7746;
XX
XX 20-NOV-2003 (first entry)
XX
XX Native CC49 heavy chain variable region.
XX
XX anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAMA; accelerated whole body clearance; mouse.
XX
XX Mus musculus.
XX
XX US6495137-B1.
XX
XX 17-DEC-2002.
XX
XX 30-OCT-1997; 97US-00961309.
XX
XX 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.

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PR 31-OCT-1996; 96US-0030173P.
XX (DOWC ) DOW CHEM CO.
PA
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
XX Padlan EA;
XX WPI; 2003-615251/58.
XX New composite and humanized anti-tumor-associated glycoprotein-72
XX monoclonal antibody useful for detecting or treating cancer.
XX Example 6; Fig 32B; 130pp; English.
XX The invention relates to a humanised or composite anti-tumour-associated
XX glycoprotein-72 (TAG-72) antibody or its fragment comprising a
XX complementarity determining region (CDR)-grafted light chain having light
XX chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
XX IV kappa light chain. The composition is suitable for the treatment and
XX detection of cancer. The novel antibody has the ability to bind
XX specifically to malignant cells and does not bind to normal cells. It
XX greatly minimises or eliminates harmful hypersensitivity anti-mouse
XX antibody (HAMA) responses. The relatively small size and human character
XX of the composite Hum4V-L, V-H single chain antibodies accelerate whole
XX body clearance, thus reducing the waiting period after injection before
XX surgery is initiated. The present sequence represents the amino acid
XX sequence of the native CC49 heavy chain variable region.
XX Sequence 115 AA;

Query Match 89.8%; Score 543; DB 6; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVVKPGASVKISKASGYTFTDTHAIHWKONPGORLEWIGVSPGNDDEKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKONPGORLEWIGVSPGNDDEKY 60

QY 61 NERFKGKATLTADTSASTAYVELSLRSDEDTAVYFCTRSLNWAYWGQGLTVTVSS 115
Db 61 NERFKGKATLTADKSSTAYVQLNSLTSDESAVYFCTRSLNWAYWGQGLTVTVSS 115

RESULT 15
ABU62751
ID ABU62751 standard; protein; 115 AA.
XX
XX AC ABU62751;
XX
XX DT 08-SEP-2003 (first entry)
XX
XX DE Murine monoclonal antibody CC49 variable heavy chain #1.
XX
XX KW Mouse; monoclonal antibody; CC49; variable heavy region; cytostatic;
XX KW vaccine; humanised antibody; tumour-associated glycoprotein 72; TAG-72;
XX KW cancer; tumour.
XX
XX OS Mus musculus.
XX
XX PN US2003004318-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 31-OCT-2001; 2001US-00998817.
XX
XX PR 31-OCT-1996; 96US-0030173P.
XX PR 30-OCT-1997; 97WO-US019641.
XX PR 18-FEB-1998; 98US-00025203.
XX
XX PA (ANDE/) ANDERSON W H K.
XX PA (TEMP/) TEMPEST P R.
XX PA (CARR/) CARR F J.
XX PA (HARR/) HARRIS W J.
XX
XX PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-491945/46.

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PA (ARMO/) ARMOUR K.
XX
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-491945/46.
XX
XX DR New humanized anti-tumor-associated glycoprotein (TAG)-72 antibodies or
XX antibody fragments, useful for treating cancers that express TAG-72, or
XX for in vivo or in vitro detection of cancer, e.g. in vivo imaging of
XX tumors or cancer cells.
XX
XX PS Claim 2; Fig 1; 41pp; English.
XX
XX CC The invention describes a humanised antibody or humanised antibody
XX fragment which specifically binds tumour-associated glycoprotein (TAG)-
XX 72. The humanised antibody or humanised antibody fragment is derived from
XX a murine antibody that binds TAG-72. The humanised anti-tumour-associated
XX glycoprotein (TAG)-72 antibodies or antibody fragments are useful for
XX treating cancers that express TAG-72, or for the in vivo or in vitro
XX detection of cancer, e.g. in vivo imaging of tumours or cancer cells that
XX express TAG-72. This is the amino acid sequence of mouse monoclonal
XX antibody CC49 variable heavy chain
XX Sequence 115 AA;

Query Match 89.8%; Score 543; DB 6; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVSGAEVVKPGASVKISKASGYTFTDTHAIHWKONPGORLEWIGVSPGNDDEKY 60
Db 1 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKONPGORLEWIGVSPGNDDEKY 60

QY 61 NERFKGKATLTADTSASTAYVELSLRSDEDTAVYFCTRSLNWAYWGQGLTVTVSS 115
Db 61 NERFKGKATLTADKSSTAYVQLNSLTSDESAVYFCTRSLNWAYWGQGLTVTVSS 115

RESULT 16
ABU62760
ID ABU62760 standard; protein; 115 AA.
XX
XX AC ABU62760;
XX
XX DT 08-SEP-2003 (first entry)
XX
XX DE Murine monoclonal antibody CC49 variable heavy chain #2.
XX
XX KW Mouse; monoclonal antibody; CC49; variable heavy region; cytostatic;
XX KW vaccine; humanised antibody; tumour-associated glycoprotein 72; TAG-72;
XX KW cancer; tumour.
XX
XX OS Mus musculus.
XX
XX PN US2003004318-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 31-OCT-2001; 2001US-00998817.
XX
XX PR 31-OCT-1996; 96US-0030173P.
XX PR 30-OCT-1997; 97WO-US019641.
XX PR 18-FEB-1998; 98US-00025203.
XX
XX PA (ANDE/) ANDERSON W H K.
XX PA (TEMP/) TEMPEST P R.
XX PA (CARR/) CARR F J.
XX PA (HARR/) HARRIS W J.
XX PA (ARMO/) ARMOUR K.
XX
XX PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-491945/46.
XX
XX DR

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XX New humanized anti-tumour-associated glycoprotein (TAG)-72 antibodies or
PT antibody fragments, useful for treating cancers that express TAG-72, or
PT for in vivo or in vitro detection of cancer, e.g. in vivo imaging of
PT tumors or cancer cells.
XX
PS Claim 2; Fig 3; 41pp; English.
XX
CC The invention describes a humanised antibody or humanised antibody
CC fragment which specifically binds tumour-associated glycoprotein (TAG)-
CC 72. The humanised antibody or humanised antibody fragment is derived from
CC a murine antibody that binds TAG-72. The humanised anti-tumour-associated
CC glycoprotein (TAG)-72 antibodies or antibody fragments are useful for
CC treating cancers that express TAG-72, or for the in vivo or in vitro
CC detection of cancer, e.g. in vivo imaging of tumours or cancer cells that
CC express TAG-72. This is the amino acid sequence of mouse monoclonal
CC antibody CC49 variable heavy chain
XX
SQ Sequence 115 AA;
Query Match 89.8%; Score 543; DB 6; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWWKQNPQRLIEWIGYFSPGNDDFKY 60
DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWWKQNPQRLIEWIGYFSPGNDDFKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNMYWGQGLTVTVSS 115
RESULT 17
AAE39057
ID AAE39057 standard; protein; 115 AA.
XX
AC AAE39057;
XX
DT 18-DEC-2003 (first entry)
XX
DE Murine CC49 VH protein.
XX
KW TAG-72; cancer; immunodetection; tumour imaging; colon carcinoma; murine;
KW CC49 antibody; VH; heavy chain variable region.
XX
OS Mus musculus.
XX
PN US2002193574-A1.
XX
PD 19-DEC-2002.
XX
PF 31-OCT-2001; 2001US-00999040.
XX
PR 31-OCT-1996; 96US-0030173P.
XX 30-OCT-1997; 97WO-US019641.
XX 18-FEB-1998; 98US-00025203.
XX (ANDE//) ANDERSON W H K.
PA (TEMP//) TEMPEST P R.
PA (CARR//) CARR F J.
PA (HARR//) HARRIS W J.
PA (ARMO//) ARMOUR K.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-644619/61.
XX
PT Humanized antibody or fragment which specifically binds TAG-72 which is a
PT pancreatic carcinoma antigen expressed by various human cancers, useful for
PT treating cancer, particularly human colon carcinoma.
XX
PS Disclosure; Page 14; 0pp; English.

XX
CC The present invention relates to a humanised antibody or its fragment
CC which specifically binds TAG-72, where the humanised antibody or its
CC fragment is derived from a murine antibody that binds TAG-72. The
CC invention is useful in in vivo treatment of cancer, particularly human
CC colon carcinoma. It is also useful in in vivo treatment of mammal having
CC a TAG-72 expressing cancer. The invention is useful in in vitro or in
CC vivo immunodetection (preferably in vivo tumour imaging) of TAG-72
CC expressing cancer cells in a mammal. The present sequence is murine CC49
CC VH (heavy chain variable region) protein. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 115 AA;
Query Match 89.8%; Score 543; DB 7; Length 115;
Best Local Similarity 89.6%; Pred. No. 2.3e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWWKQNPQRLIEWIGYFSPGNDDFKY 60
DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHWWKQNPQRLIEWIGYFSPGNDDFKY 60
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVYFCTSLNMYWGQGLTVTVSS 115
DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNMYWGQGLTVTVSS 115
RESULT 18
ADG46866
ID ADG46866 standard; protein; 115 AA.
XX
AC ADG46866;
XX
DT 11-MAR-2004 (first entry)
XX
DE Murine CC49 VH protein.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; mouse.
XX
OS Mus musculus.
XX
PN US2003165498-A1.
XX
PD 04-SEP-2003.
XX
PF 25-SEP-2002; 2002US-00255478.
XX
PR 19-APR-1990; 90US-00510697.
XX 20-OCT-1992; 92US-00964536.
XX 16-JUN-1994; 94US-00261354.
XX 31-OCT-1996; 96US-0030173P.
XX 30-OCT-1997; 97US-00961309.
XX (MEZE//) MEZES P S.
PA (RICH//) RICHARD R A.
PA (JOHN//) JOHNSON K S.
PA (SCHL//) SCHLOM J.
PA (KASH//) KASHMIRI S V S.
PA (SHUL//) SHU L.
PA (PADL//) PADLAN E A.
XX
PI Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
XX Padlan EA;
XX
DR WPI; 2003-898033/82.
XX
PT New humanized or composite anti-TAG-72 monoclonal antibody with subgroup
PT IV kappa light chain framework regions, useful in the fields of
PT immunology and genetic engineering, particularly for detecting and/or
PT treating cancer.

XX Disclosure; SEQ ID NO 74; 133pp; English.

XX The invention relates to a humanised or composite anti-tumour-associated

CC glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody

CC comprises a complementarity determining region (CDR)-grafted light chain

CC having non-human CDRs grafted to a human subgroup IV kappa light chain.

CC The invention is useful in gene-therapy. The methods and compositions of

CC the present invention are useful in the fields of immunology and genetic

CC engineering, particularly for detecting and/or treating cancer. The

CC present sequence is murine CC49 VH protein used in the exemplification of

CC the invention.

XX SQ Sequence 115 AA;

Query Match 89.8%; Score 543; DB 7; Length 115;

Best Local Similarity 89.6%; Pred. No. 2.3e-41;

Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNPQGRLEWIGYFSPGNDPFKY 60

DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHVKQNPQGRLEWIGYFSPGNDPFKY 60

QY 61 NERFKGKATLTADTSNSTAYVELSLRSEDYAVYFCTRSLSNAYWGQGTLTVTSS 115

DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLSNAYWGQGTSTVTSS 115

RESULT 19

ADP71403

ID ADP71403 standard; protein; 115 AA.

XX AC ADP71403;

XX DT 12-FEB-2004 (first entry)

DE Mouse CC49 heavy chain variable region protein.

XX antibody; tumour; glycoprotein TAG-72; cancer; CC49;

KW heavy chain variable region; murine; mouse.

XX Mus sp.

OS US2002183497-A1.

PN 05-DEC-2002.

PD 31-OCT-2001; 2001US-00999025.

XX 31-OCT-1996; 96US-0030173P.

PR 30-OCT-1997; 97WO-US019641.

PR 18-FEB-1998; 98US-00025203.

XX (ANDE/) ANDERSON W H K.

PA (TEMP/) TEMPEST P R.

PA (CARR/) CARR F J.

PA (HARR/) HARRIS W J.

PA (ARMO/) ARMOUR K.

XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;

PI WPI; 2004-068735/07.

XX Humanized antibody or antibody fragment which specifically binds tumor

PT associated glycoprotein TAG-72 is useful to detect TAG-72 expressing

PT cancer cells in vitro or in vivo for subsequent excision.

XX Example 1; Fig 3; 29pp; English.

PS The invention relates to a novel humanised antibody or antibody fragment

CC which specifically binds a tumour associated glycoprotein TAG-72 and is

CC derived from a murine antibody that binds TAG-72. The invention further

CC relates to: a nucleic acid sequence from which may be expressed the novel

CC antibody which comprises complementarity determining regions (CDRs)

CC obtained from the murine antibody Variable Heavy Framework Regions (FRe)

CC which have an amino acid sequence of the NEMM FR or the humanised CC49

CC FRs as shown in the specification and Variable Light FRs which have an

CC amino acid sequence of the REI FRs or the humanised CC49 FRs shown in the

CC specification; a vector comprising the nucleic acid of glycoprotein TAG-

CC 72; a composition for treating cancer comprising the novel antibody; in

CC vivo treatment of a mammal having a TAG-72-expressing cancer comprising

CC administering the composition; in vitro immunodetection of TAG-72-

CC expressing cancer cells comprising contacting the cells with the

CC composition where the antibody is associated with or linked to a

CC detectable label; treating cancer comprising: intravenously administering

CC the novel radionuclide-labelled antibody; detecting tumour cells using a

CC radionuclide probe; and removing the detected tumour cells by surgical

CC incision. The invention is useful to detect TAG-72 expressing cancer

CC cells in vitro or in vivo for subsequent excision. This sequence

CC represents a mouse CC49 heavy chain variable region protein of the

CC invention.

XX SQ Sequence 115 AA;

Query Match 89.8%; Score 543; DB 8; Length 115;

Best Local Similarity 89.6%; Pred. No. 2.3e-41;

Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKQNPQGRLEWIGYFSPGNDPFKY 60

DB 1 QVQLQSDAELVKPGASVKISKASGYTFTDHAHHVKQNPQGRLEWIGYFSPGNDPFKY 60

QY 61 NERFKGKATLTADTSNSTAYVELSLRSEDYAVYFCTRSLSNAYWGQGTLTVTSS 115

DB 61 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLSNAYWGQGTSTVTSS 115

RESULT 20

AR04383

ID AAR04383 standard; protein; 134 AA.

XX AC AAR04383;

XX DT 09-SEP-2004 (revised)

DT 25-MAR-2003 (revised)

DT 13-SEP-1990 (first entry)

XX DE Colon Cancer monoclonal antibody CC49 heavy chain variable region.

XX chimeric antibodies; TAG72; light chain variable region;

KW heavy chain variable region; ss; colon cancer.

XX Synthetic.

OS Key Location/Qualifiers

FT Peptide 1..19

FT Region /note= "leader peptide"

FT Region 50..54

FT Region /note= "hypervariable region 1"

FT Region 69..85

FT Region /note= "hypervariable region 2"

FT Region 104..109

FT Region /note= "hypervariable region 3"

XX EP365997-A.

XX PD 02-MAY-1990.

XX PF 18-OCT-1989; 89EP-00119361.

XX PR 19-OCT-1988; 88US-00259943.

XX (DOWC) DOW CHEM CO.

XX Mezes P, Gourlie B, Rixon M;

XX

DR WPI; 1990-133521/18.
DR N-PSDB; AAQ04259.
XX
PT Chimeric antibodies against tag 72 - and conjugate to provide imaging
PT markers and therapeutic tools.
XX
PS Disclosure; Page ?; 2pp; English.
XX
CC The polypeptide forms part of a chimera. The other components are a light
CC chain variable region and human-derived constant light and heavy chain
CC regions. The variable regions have high affinity for TAG72. The constant
CC regions reduce the side-effects when administered to human patients
CC because they are of human origin. See also AAR04381-2 and AAR04384-8.
CC (Updated on 25-MAR-2003 to correct PA field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to pages and features
XX
SQ Sequence 134 AA;

Query Match 89.8%; Score 543; DB 2; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.7e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNFQGLRWIGYFSPGNDDPKY 60
DB 20 QVQLQQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNFQGLRWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSLNMYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGLTVTVSS 134

RESULT 21
AAI50685
ID AAY50685 standard; protein; 134 AA.
AC AAY50685;
XX
DT 09-FEB-2000 (first entry)
XX
DE Human CC49 protein.
XX
KW Human; antibody; humanized; anti-tumor; sialylated glycoprotein antibody;
KW TAG-72; cytostatic; cancer antigen; detection; carcinoma lesion;
KW diagnostic; treatment.
XX
OS Homo sapiens.
XX
FN US5976531-A.
XX
PD 02-NOV-1999.
XX
PF 16-JUN-1994; 94US-00261354.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
XX
PA (DOWC) DOW CHEM CO.
XX
FI Johnson KS, Mezes PS, Richard RA;
XX
DR WPI; 1999-632731/54.
XX
PT New humanized anti-TAG-72 antibodies, used for the detection, in vivo
PT imaging and treatment of cancers.
XX
PS Disclosure; Fig 3A-E; 83pp; English.
XX
CC This invention describes novel humanized anti-tumor associated sialylated
CC glycoprotein antibodies (TAG-72) which have cytostatic activity. The
CC antibodies have binding specificity for the cancer antigen TAG-72. They
CC can be used for the in vivo detection of carcinoma lesions. They can also
CC be used for in vitro diagnostics. They can also be modified with

CC therapeutic agents e.g. a radionuclide, drug, biological response
CC modifier, toxin or another antibody for the treatment of cancers. The
CC humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC hypersensitivity reactions
XX
SQ Sequence 134 AA;

Query Match 89.8%; Score 543; DB 2; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.7e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWVKQNFQGLRWIGYFSPGNDDPKY 60
DB 20 QVQLQQSDAELVKPGASVKISKASGYTFTDTHAIHWVKQNFQGLRWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTSASTAYVELSLRSEDYAVFCTRSLNMYWGQGLTVTVSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNMYWGQGLTVTVSS 134

RESULT 22
AAI57176
ID AAY57176 standard; protein; 134 AA.
XX
AC AAY57176;
XX
DT 29-FEB-2000 (first entry)
XX
DE Amino acid sequence of CC49 VH region.
XX
KW Tumor associated sialylated glycoprotein; TAG-72; cancer antigen;
KW carcinoma lesion; diagnostic; cancer; antibody; human; CC49;
KW anti-mouse antibody hypersensitivity reaction.
XX
OS Homo sapiens.
XX
FN US5976845-A.
XX
PD 02-NOV-1999.
XX
PF 07-JUN-1995; 95US-00487743.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
XX
PA (DOWC) DOW CHEM CO.
XX
FI Johnson KS, Richard RA, Mezes PS;
XX
DR WPI; 1999-619651/53.
DR N-PSDB; AAZ39424.

Production of humanized anti-TAG-72 antibodies, used for the detection,
in vivo imaging and treatment of cancers.
XX
PS Disclosure; Fig 3A-E; 85pp; English.
XX
CC The invention relates to producing humanized anti-tumor associated
CC sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies
CC have binding specificity for the cancer antigen TAG-72. These antibodies
CC have variable regions with VL segments derived from human subgroup IV
CC germline gene and a VH segment (encoded by the Vhalphatag germline gene)
CC which is capable of combining with the VL to form a three dimensional
CC structure having the ability to bind TAG-72. They can be used for the in
CC vivo detection of carcinoma lesions. They can also be used for in vitro
CC diagnostics. They can also be modified with therapeutic agents e.g. a
CC radionuclide, drug, biological response modifier, toxin or another
CC antibody for the treatment of cancers. The humanized anti-TAG-72
CC antibodies can reduce harmful anti-mouse antibody hypersensitivity
XX
SQ Sequence 134 AA;

Query Match 89.8%; Score 543; DB 2; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.7e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQGLRWIGYFSPGNDPKY 60
DB 20 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQGLRWIGYFSPGNDPKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTSLNNMAYGQGTSLVTSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNNMAYGQGTSLVTSS 134

RESULT 23
AA57047
ID AAY57047 standard; protein; 134 AA.
XX AC AAY57047;
XX DT 21-FEB-2000 (first entry)
XX DE Amino acid sequence of antibody CC49 heavy chain variable region.
XX KW VhalphatAG; anti-tumour associated sialylated glycoprotein antigen;
XX KW TAG-72; variable region; heavy chain; carcinoma; detect; tumour;
XX KW mouse-human chimeric antibody; therapeutic agent; intraoperative therapy.
XX OS Mus sp.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "Putative signal peptide"
FT Protein 20..134
FT Protein /note= "Putative mature peptide"
XX US5993813-A.
XX PD 30-NOV-1999.
XX PF 24-MAR-1997; 97US-00822028.
XX PR 19-OCT-1988; 88US-00259943.
XX PR 24-OCT-1988; 88US-00261942.
XX PR 19-OCT-1989; 89US-00424362.
XX PR 31-MAR-1993; 93US-00040687.
XX PA (DOWC) DOW CHEM CO.
XX PI Mezes PS, Gourlie BB, Schlom J, Kaplan DA, Anderson WHK;
XX PI Rixon MW;
XX DR WPI; 2000-038240/03.
XX DR N-PSDB; AA240702.
XX PT New mouse-human chimeric antibody, useful for in vivo diagnosis of cancer.
XX PS Example; Fig 3; 120pp; English.
XX CC AA57047-257050 are heavy chain variable region amino acid sequences from monoclonal antibodies directed against TAG-72, designated colon cancer (CC) antibodies. These antibody regions are produced from the rearrangement of VhalphatAG (AA240701). The antibodies are used in the invention which relates to a new anti-tumour associated sialylated glycoprotein antigen (TAG)-72 mouse-human chimeric antibody. The variable region of the antibody has a heavy chain (VH) where VH is encoded by a DNA sequence homologous to the VhalphatAG germline gene. The invention includes a method for in vivo carcinoma targeting through the administration to an animal of an anti-TAG-72 mouse-human chimeric antibody produced by specific cell lines. The antibody or a fragment are conjugated to an imaging marker or therapeutic agent, in a pharmaceutically acceptable, nontoxic, sterile carrier. The chimeric

CC antibody binds to TAG-72 which is found on certain human tumour cells.
CC The tissue regions containing the tumours can be detected via the markers
CC and/or can be treated via the therapeutic agents. The method is useful
CC for in vivo diagnosis and treatment of cancer by administering to an
CC animal an effective amount of a composition for the in situ detection of
CC carcinoma lesions. The method is useful for intraoperative therapy,
CC consisting of locating the position of a tumour through the
CC administration of the antibody, followed by excising the tumour
XX SQ Sequence 134 AA;
XX Query Match 89.8%; Score 543; DB 3; Length 134;
XX Best Local Similarity 89.6%; Pred. No. 2.7e-41;
XX Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQGLRWIGYFSPGNDPKY 60
DB 20 QVQLQSDAELVKPGASVKISKASGYTFTDTHAIHWKQNPQGLRWIGYFSPGNDPKY 79

QY 61 NERFKGKATLTADTSASTAYVELSLRSEDVAVYFCTSLNNMAYGQGTSLVTSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTSLNNMAYGQGTSLVTSS 134

RESULT 24
AA570715
ID AAY90715 standard; protein; 134 AA.
XX AC AAY90715;
XX DT 14-AUG-2000 (first entry)
XX DE CC49 VH region protein sequence SEQ ID NO:4.
XX KW Chimeric antibody; VhalphatAG; TAG-72; human; mouse; diagnosis;
XX KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;
XX KW cancer; detection; therapy.
XX OS Homo sapiens.
XX OS Mus sp.
XX PN US6051225-A.
XX PD 18-APR-2000.
XX PF 31-MAR-1993; 93US-00040687.
XX PR 19-OCT-1988; 88US-00259943.
XX PR 24-OCT-1988; 88US-00261942.
XX PR 19-OCT-1989; 89US-00424362.
XX PA (DOWC) DOW CHEM CO.
XX PI Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;
XX PI Rixon MW;
XX DR WPI; 2000-349294/30.
XX DR N-PSDB; AAA29683.
XX PT Novel family of chimeric antibodies for treating cancer with high
XX PT affinities to a high molecular weight tumor-associated sialylated
XX PT glycoprotein antigen of human origin.
XX PS Example; Fig 3; 122pp; English.
XX CC The present invention describes an antibody (I) produced by one of the
XX CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4
XX CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC
XX CC HB9876); CH88-4 (ATCC HB9874); CH84-1 (ATCC HB9883); CH84-2 (ATCC HB9879)
XX CC ; CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to
XX CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at
XX CC least 25% greater than B72.3. (I) can be used for treating and diagnosing
XX CC cancer, and for the in situ detection of carcinoma lesions and for in

CC vivo therapy. AAA29682 to AAA29744, and AAY90714 to AAY90723, represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 134 AA;

Query Match 89.8%; Score 543; DB 3; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.7e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTTQDAIHVWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLQQSDAELVKPGASVKISKASGYFTTQDAIHVWKQNPQORLEWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTTSASTAYVELSLRSEDPAVYFCTRSLNWAYWGQGTSLTVSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNWAYWGQGTSLTVSS 134

RESULT 25
AAY90722
ID AAY90722 standard; protein; 134 AA.
XX
AC AAY90722;
XX
DT 14-AUG-2000 (first entry)
XX
DE CC49 VH region CNBr amino acid sequence SEQ ID NO:29.
XX
KW Chimeric antibody; VhalphaTAG; TAG-72; human; mouse; diagnosis;
KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;
KW cancer; detection; therapy.
XX
OS Homo sapiens.
OS Mus sp.
XX
PN US6051225-A.
XX
PD 18-APR-2000.
XX
PF 31-MAR-1993; 93US-00040687.
XX
PR 19-OCT-1988; 88US-00259943.
PR 24-OCT-1988; 88US-00261942.
PR 19-OCT-1989; 89US-00424362.
XX
PA (DOWC) DOW CHEM CO.
XX
PI Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;
PI Rixon MW;
XX
DR WPI; 2000-349294/30.
XX
PT Novel family of chimeric antibodies for treating cancer with high
PT affinities to a high molecular weight tumor-associated sialylated
PT glycoprotein antigen of human origin.
XX
PS Example; Fig 18; 122pp; English.
XX
CC The present invention describes an antibody (I) produced by one of the
CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4
CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC
CC HB9876); CH88-4 (ATCC HB9874); CH84-1 (ATCC HB9883); CH84-2 (ATCC HB9879)
CC ; CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to
CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at
CC least 25% greater than B72.3. (I) can be used for treating and diagnosing
CC cancer, and for the in situ detection of carcinoma lesions and for in
CC vivo therapy. AAA29682 to AAA29744, and AAY90714 to AAY90723, represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 134 AA;

Query Match 89.8%; Score 543; DB 3; Length 134;
Best Local Similarity 89.6%; Pred. No. 2.7e-41;
Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Matches 103; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVVKPGASVKISKASGYFTTQDAIHVWKQNPQORLEWIGYFSPGNDDPKY 60
DB 20 QVQLQQSDAELVKPGASVKISKASGYFTTQDAIHVWKQNPQORLEWIGYFSPGNDDPKY 79
QY 61 NERFKGKATLTADTTSASTAYVELSLRSEDPAVYFCTRSLNWAYWGQGTSLTVSS 115
DB 80 NERFKGKATLTADKSSSTAYVQLNSLTSEDSAVYFCTRSLNWAYWGQGTSLTVSS 134

Search completed: July 25, 2005, 07:56:16
Job time : 125.031 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	540	91.2	113	2	A49260	antitumor monoclon	
2	530.5	89.6	118	2	PT0356	Ig kappa chain V r	
3	528.5	89.3	138	2	S26040	Ig kappa chain pre	
4	527	89.0	114	1	K4HULN	Ig kappa chain V-I	
5	527	89.0	145	2	PL0014	Ig kappa chain pre	
6	526	88.9	113	2	S30520	Ig kappa chain V r	
7	523	88.3	134	2	S49531	anti-Sm antibody V	
8	520	87.8	240	2	S06084	Ig kappa chain pre	
9	519	87.7	113	2	S34002	Ig kappa chain V r	
10	517	87.3	114	2	S44119	Ig kappa chain V-J	
11	516	87.2	114	2	S44116	Ig kappa chain V-J	
12	514	86.8	113	2	PL0263	Ig kappa chain V r	
13	513	86.7	120	2	S51147	antibody light cha	
14	513	86.7	134	1	K4HU17	Ig kappa chain pre	
15	512.5	86.6	112	2	S09370	Ig kappa chain V-J	
16	512.5	86.6	133	1	K4HUJ1	Ig kappa chain pre	
17	511	86.3	134	2	PC1214	Ig kappa chain pre	
18	508	85.8	113	2	S34003	Ig kappa chain V r	
19	506	85.5	129	2	S40347	Ig kappa chain - h	
20	502	84.8	113	2	S30523	Ig kappa chain V r	
21	502	84.8	124	2	S40364	Ig kappa chain - h	
22	498	84.1	112	2	F30538	Ig kappa chain V r	
23	496	83.8	132	2	S46373	Ig kappa chain V-J	
24	495.5	83.7	112	2	S41393	Ig kappa chain V r	
25	495	83.6	112	2	E30538	Ig kappa chain V r	
26	489	82.6	113	2	PL0264	Ig kappa chain V r	
27	487.5	82.3	112	2	PL0265	Ig kappa chain V r	
28	486	82.1	220	2	A31790	Ig kappa chain V r	
29	484.5	81.8	138	2	A53261	Ig kappa chain pre	

Db 1 DIVMTQSPNSLAVSLGERATINCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60
Qy 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 114
Db 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLEIKR 114

RESULT 5
PL0014
Ig kappa chain precursor V region (F6-3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0014
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0014
A;Molecule type: mRNA
A;Residues: 1-145 <CHE>
A;Experimental source: cell line F6-3
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-134/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F;36-116/Domain: immunoglobulin homology <IMM>
F;44-60/Region: complementarity-determining 1
F;76-82/Region: complementarity-determining 2
F;115-123/Region: complementarity-determining 3
F;135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match 89.0%; Score 527; DB 2; Length 145;
Best Local Similarity 86.0%; Pred. No. 3.3e-40;
Matches 98; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSLAVSLGERVTLNCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60
Db 21 DIVMTQSPDLSLAVSLGERVTLNCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 80

Qy 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLEMR 134

RESULT 6
S30520
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S30520
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAR>
A;Cross-references: EMBL:Z18325
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 88.9%; Score 526; DB 2; Length 113;
Best Local Similarity 86.7%; Pred. No. 3.2e-40;
Matches 98; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSLAVSLGERVTLNCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60
Db 1 DIVMTQSPDLSLAVSLGERATINCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60

Qy 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 113

Db 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKVEIK 113

RESULT 7
S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C;Accession: S49531
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49531
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <NAH>
A;Cross-references: EMBL:Z46347; NID:G560841; PIDN:CAA86466.1; PID:G560842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 523; DB 2; Length 134;
Best Local Similarity 86.0%; Pred. No. 7e-40;
Matches 98; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSLAVSLGERVTLNCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60
Db 21 DIVMTQSPDLSLAVSLGERATINCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 80

Qy 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKVDIKR 134

RESULT 8
S06084
Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 1992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A;Reference number: S06084; MUID:90016888; PMID:2508067
A;Accession: S06084
A;Molecule type: mRNA
A;Residues: 1-240 <CRO>
A;Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 520; DB 2; Length 240;
Best Local Similarity 86.0%; Pred. No. 2.3e-39;
Matches 98; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIVMTQSPDLSLAVSLGERVTLNCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 60
Db 21 DIVMTQSPDLSLAVSAGETVTINCKSSQSLVYSSNKNYLAHYQKQPKPQLLIYWASTR 80

Qy 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 114
Db 81 QSGVDPDRFSGSGGTDTLTITSSVQAEADVAVYVYCOQYYSYPLTFGAGTKLELKR 134

RESULT 9
S34002
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34002; S30522

F:16-96/Domain: immunoglobulin homology <IMM>

A;Reference number: PC121

A;Reference number: PCI213; MUID:93077049; PMID:1446832

S41393
IG kappa chain V region (12.5H VL) - mouse
C:Species: Mus musculus (house mouse)
C:date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S41393
R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, P.
submitted to the EMBL Data Library, January 1994

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1	587	99.2	113	14	US-10-255-478-73	Sequence 73, Appl
2	581	91.4	134	14	US-10-235-478-58	Sequence 58, Appl
3	540	91.2	113	9	US-09-999-023-7	Sequence 7, Appl
4	540	91.2	113	9	US-09-999-025-13	Sequence 13, Appl
5	540	91.2	113	9	US-09-999-040-7	Sequence 7, Appl
6	540	91.2	113	9	US-09-999-040-13	Sequence 13, Appl
7	540	91.2	113	10	US-09-998-817-7	Sequence 7, Appl
8	540	91.2	113	10	US-09-998-817-13	Sequence 13, Appl
9	540	91.2	113	10	US-09-999-021-7	Sequence 7, Appl
10	540	91.2	113	10	US-09-999-021-13	Sequence 13, Appl
11	540	91.2	113	14	US-10-040-597-7	Sequence 7, Appl

85 528 89.2 135 14 US-10-171-452A-1 Sequence 1, Appli
86 528 89.2 135 15 US-10-353-708-1 Sequence 1, Appli
87 528 89.2 135 16 US-10-731-984-35 Sequence 35, Appl
88 528 89.2 179 17 US-10-644-277-140 Sequence 140, Appl
89 527 89.0 113 9 US-09-274-163E-16 Sequence 16, Appli
90 527 89.0 114 9 US-09-274-163E-4 Sequence 4, Appli
91 526 88.9 264 15 US-10-264-049-4274 Sequence 4274, Ap
92 525.5 88.8 130 13 US-10-146-305-7 Sequence 7, Appli
93 525 88.7 113 10 US-09-995-529-6 Sequence 6, Appli
94 525 88.7 113 11 US-09-995-529-6 Sequence 6, Appli
95 524 88.5 122 14 US-10-010-729-51 Sequence 51, Appli
96 524 88.5 240 9 US-09-799-514-8 Sequence 8, Appli
97 523 88.3 114 9 US-09-749-831-16 Sequence 16, Appli
98 523 88.3 114 17 US-10-483-994-8 Sequence 8, Appli
99 523 88.3 114 17 US-10-483-993-8 Sequence 8, Appli
100 523 88.3 114 17 US-10-706-689-15 Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-10-255-478-73
; Sequence 73, Application US/10255478
; Publication No. US20030165498A1
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padian, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/10/255,478
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/08/961,309
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 08/261,354
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: US 07/964,536
; PRIOR FILING DATE: 1992-10-20
; PRIOR APPLICATION NUMBER: US 07/510,697
; PRIOR FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 73
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Hucc49 VL
; LOCATION: 1..113
; OTHER INFORMATION: Humanized CC49 light chain variable region with Hum4 VL FRs
; FEATURE:
; NAME/KEY: LEN FR1
; LOCATION: 1..23
; OTHER INFORMATION: Human LEN light chain variable region FR1
; FEATURE:
; NAME/KEY: CC49 VL CDR1
; LOCATION: 24..40
; OTHER INFORMATION: Murine CC49 light chain variable region CDR1
; FEATURE:
; NAME/KEY: LEN FR2
; LOCATION: 41..55
; OTHER INFORMATION: Human LEN light chain variable region FR2
; FEATURE:
; NAME/KEY: CC49 VL CDR2
; LOCATION: 56..62

; OTHER INFORMATION: Murine CC49 light chain variable region CDR2
; FEATURE:
; NAME/KEY: LEN FR3
; LOCATION: 63..94
; OTHER INFORMATION: Human LEN light chain variable region FR3
; FEATURE:
; NAME/KEY: CC49 VL CDR3
; LOCATION: 95..103
; OTHER INFORMATION: Murine CC49 light chain variable region CDR3
; FEATURE:
; NAME/KEY: LEN FR4
; LOCATION: 104..113
; OTHER INFORMATION: Human LEN light chain variable region FR4
US-10-255-478-73
Query Match 99.2%; Score 587; DB 14; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.5e-45;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTLTITSSVQAEDVAVYCCQYYSYPLTFTGAGTKLELK 113
Db 61 ESGVDPDRFSGSGGTDTLTITSSVQAEDVAVYCCQYYSYPLTFTGAGTKLELK 113
RESULT 2
US-10-255-478-58
; Sequence 58, Application US/10255478
; Publication No. US20030165498A1
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padian, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 37777E
; CURRENT APPLICATION NUMBER: US/10/255,478
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/08/961,309
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 08/261,354
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: US 07/964,536
; PRIOR FILING DATE: 1992-10-20
; PRIOR APPLICATION NUMBER: US 07/510,697
; PRIOR FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 58
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Hum4 VL
; LOCATION: 1..134
US-10-255-478-58
Query Match 91.4%; Score 541; DB 14; Length 134;
Best Local Similarity 88.6%; Pred. No. 2.6e-41;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQKPGQSPKLLIYWASAR 60
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; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-09-999-025-13

Query Match          91.2%; Score 540; DB 9; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPSLAVSLGERTVLTCKSSQSLLYSGNQKNYLAWYQOKPGQSKLLIYWASAR 60
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QY 61 ESGVPRFRFGSGSGTGDTFLTITSSVQAEADVAVVYCCQVYSYPLTFGAGTKLELK 113
DB 61 ESGVPRFRFGSGSGTGDTFLTITSSVQAEADVAVVYCCQVYSYPLTFGAGTKLVLK 113

RESULT 5
US-09-999-040-7
; Sequence 7, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
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; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VK
; LOCATION: 1..113
US-09-999-040-7

Query Match          91.2%; Score 540; DB 9; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPSLAVSLGERTVLTCKSSQSLLYSGNQKNYLAWYQOKPGQSKLLIYWASAR 60
DB 1 DIVMSQSPSLPVSVEGKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSKLLIYWASAR 60

QY 61 ESGVPRFRFGSGSGTGDTFLTITSSVQAEADVAVVYCCQVYSYPLTFGAGTKLELK 113
DB 61 ESGVPRFRFGSGSGTGDTFLTITSSVQAEADVAVVYCCQVYSYPLTFGAGTKLVLK 113

RESULT 6
US-09-999-040-13
; Sequence 13, Application US/09999040
; Publication No. US20020193574A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr

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; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 09/999,040
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
; US-09-999-040-13

Query Match
Best Local Similarity 91.2%; Score 540; DB 9; Length 113;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Db 1 DIVMSQSPSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGTDFLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVDPDRFTGSGSGTDFLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 8
US-09-998-817-13
; Sequence 13, Application US/09998817
; Publication No. US20030004318A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/998,817
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US/09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: FILING DATE: 1997-10-30
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; PRIOR FILING DATE: FILING DATE: 1996-10-31
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; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
; US-09-998-817-13

Query Match
Best Local Similarity 91.2%; Score 540; DB 10; Length 113;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPSLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVDPDRFTGSGSGTDFLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 9
US-09-999-021-7
; Sequence 7, Application US/09999021
; Publication No. US20030013854A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Cart, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
```



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; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VK
; LOCATION: 1..113
US-09-999-021-7

Query Match          91.2%; Score 540; DB 10; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
DB 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113

RESULT 10
US-09-999-021-13
; Sequence 13, Application US/09999021
; Publication No. US20030013854A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-09-999-021-13

Query Match          91.2%; Score 540; DB 10; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
DB 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113

RESULT 11
US-09-999-021-13
; Sequence 13, Application US/09999021
; Publication No. US20030013854A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-09-999-021-13

Query Match          91.2%; Score 540; DB 10; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
DB 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113

RESULT 12
US-10-040-997-13
; Sequence 13, Application US/10040997
; Publication No. US20030013856A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/040,997
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-10-040-997-13

Query Match          91.2%; Score 540; DB 14; Length 113;
Best Local Similarity 90.3%; Pred. No. 2.7e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
DB 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTLTITSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113
```



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Publication No. US20030212027A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; TITLE OF INVENTION: Vaccine Formulations and Methods for Immunizing an
; TITLE OF INVENTION: Individual Against Shed Antigen-Specific B Cells
; FILE REFERENCE: 26983-46-1
; CURRENT APPLICATION NUMBER: US/10/336,210
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 60/139,521
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 09/594,985
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
; US-10-336-210-6

Query Match          91.2%; Score 540; DB 15; Length 271;
Best Local Similarity 90.3%; Pred. No. 6.8e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGSRVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 159 DIVMSQSPSSLPVSVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 218

Qy 61 ESGVPRFSGSGSDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 219 ESGVPRFTGSGSDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 271

RESULT 17
US-10-336-210-7
; Sequence 7, Application US/10336210
; Publication No. US20030212027A1
; GENERAL INFORMATION:
; APPLICANT: Barbera-Guillem, Emilio
; APPLICANT: Nelson, M. Bud
; TITLE OF INVENTION: Vaccine Formulations and Methods for Immunizing an
; TITLE OF INVENTION: Individual Against Shed Antigen-Specific B Cells
; FILE REFERENCE: 26983-46-1
; CURRENT APPLICATION NUMBER: US/10/336,210
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 60/139,521
; PRIOR FILING DATE: 1999-06-16
; PRIOR APPLICATION NUMBER: 09/594,985
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
; US-10-336-210-7

Query Match          91.2%; Score 540; DB 15; Length 272;
Best Local Similarity 90.3%; Pred. No. 6.8e-41;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGSRVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 160 DIVMSQSPSSLPVSVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 219

Qy 61 ESGVPRFSGSGSDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 220 ESGVPRFTGSGSDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 272
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```
RESULT 18
US-10-013-173-49
; Sequence 49, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C1
; CURRENT APPLICATION NUMBER: US/10/013,173
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for the CC49 single
; OTHER INFORMATION: chain antibody-genomic streptavidin fusion
; US-10-013-173-49

Query Match          91.2%; Score 540; DB 14; Length 444;
Best Local Similarity 90.3%; Pred. No. 1.1e-40;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGSRVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 166 DIVMSQSPSSLPVSVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 225

Qy 61 ESGVPRFSGSGSDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 226 ESGVPRFTGSGSDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 278
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```
RESULT 19
US-10-150-762-49
; Sequence 49, Application US/10150762
; Publication No. US20030103948A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen C.
; APPLICANT: Graves, Scott S.
; APPLICANT: Schultz, Joanne E.
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James A.
; APPLICANT: Reno, Jonh M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 690022.547C2
; CURRENT APPLICATION NUMBER: US/10/150,762
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for the CC49 single
; OTHER INFORMATION: chain antibody-genomic streptavidin fusion
; US-10-150-762-49

Query Match          91.2%; Score 540; DB 14; Length 444;
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```
Best Local Similarity 90.3%; Pred. No. 1.1e-40;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 166 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 225

QY 61 ESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 226 ESGVDPFRFSGSGGTDFTLTISVKTEDLAVYCCQYYSYPLTFGAGTKLVLK 278

RESULT 20
US-10-244-821-49
; Sequence 49, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
; APPLICANT: Goshorn, Stephen Charles
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Schultz, Joanne Elaine
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Dearstyne, Erica A.
; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
; FILE REFERENCE: 690022.547C3
; CURRENT APPLICATION NUMBER: US/10/244,821
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted amino acid sequence for the CC49 single
; OTHER INFORMATION: chain antibody-genomic streptavidin fusion
; OTHER INFORMATION: sequence
US-10-244-821-49

Query Match 91.2%; Score 540; DB 14; Length 444;
Best Local Similarity 90.3%; Pred. No. 1.1e-40;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 166 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 225

QY 61 ESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 226 ESGVDPFRFSGSGGTDFTLTISVKTEDLAVYCCQYYSYPLTFGAGTKLVLK 278

RESULT 21
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
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; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 91.0%; Score 539; DB 9; Length 240;
Best Local Similarity 88.6%; Pred. No. 7.3e-41;
Matches 101; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQKPGQPPKLLIFWASTR 80

QY 61 ESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPFRFSGSGGTDFTLTISLQAEADVAVYCCQYYSYPLTFGQGTKEIKR 134

RESULT 22
US-10-159-006-36
; Sequence 36, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-36

Query Match 91.0%; Score 539; DB 14; Length 240;
Best Local Similarity 88.6%; Pred. No. 7.3e-41;
Matches 101; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDSLAVSLGERATINCKSSQSLLYSRNQKNYLAWYQKPGQPPKLLIFWASTR 80

QY 61 ESGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPFRFSGSGGTDFTLTISLQAEADVAVYCCQYYSYPLTFGQGTKEIKR 134

RESULT 23
US-09-791-578-6
; Sequence 6, Application US/09791578
; Patent No. US20020061307A1
; GENERAL INFORMATION:
; APPLICANT: WHITLOW, MARC
; APPLICANT: SHORR, ROBERT G. L.
; APPLICANT: FILPUILA, DAVID R.
; APPLICANT: LEE, LIHSYNG S.
; TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
```

;/ POLYPEPTIDES
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;/ STREET: 1100 NEW YORK AVENUE, SUITE 600
;/ CITY: WASHINGTON
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ FILING DATE: 26-Feb-2001
;/ APPLICATION NUMBER: US/09/791,578
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/069,842
;/ FILING DATE: <Unknown>
;/ APPLICATION NUMBER: US 60/050,472
;/ FILING DATE: 23-JUN-1997
;/ APPLICATION NUMBER: US 60/063,074
;/ FILING DATE: 27-OCT-1997
;/ APPLICATION NUMBER: US 60/067,341
;/ FILING DATE: 02-DEC-1997
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: JORGE A. GOLDSTEIN
;/ REGISTRATION NUMBER: 29,021
;/ REFERENCE/DOCKET NUMBER: 0977.1840002
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-371-2600
;/ TELEFAX: 202-371-2540
;/ INFORMATION FOR SEQ ID NO: 6:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 241 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;/ US-09-791-578-6
;/
;/ Query Match 91.0%; Score 539; DB 9; Length 241;
;/ Best Local Similarity 89.4%; Pred. No. 7.4e-41;
;/ Matches 101; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
;/
;/ Qy 1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLYSQKKNYLAWYQKQSPKLLIYWASAR 60
;/ Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLYSQKKNYLAWYQKQSPKLLIYWASAR 60
;/
;/ Qy 61 ESGVPRFSGSGSDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
;/ Db 61 ESGVPRFTGSGSDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113
;/
;/ RESULT 24
;/ US-09-791-540-6
;/ Sequence 6, Application US/09791540
;/ Patent No. US20020098192A1
;/ GENERAL INFORMATION:
;/ APPLICANT: WHITLOW, MARC
;/ SHORR, ROBERT G.L.
;/ FILPULA, DAVID R.
;/ LEE, LIHSYNG S.
;/ TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;/ STREET: 1100 NEW YORK AVENUE, SUITE 600
;/ CITY: WASHINGTON
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.30

;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ FILING DATE: 26-Feb-2001
;/ APPLICATION NUMBER: US/09/791,540
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 09/069,842
;/ FILING DATE: 1998-04-30
;/ APPLICATION NUMBER: US 60/050,472
;/ FILING DATE: 23-JUN-1997
;/ APPLICATION NUMBER: US 60/063,074
;/ FILING DATE: 27-OCT-1997
;/ APPLICATION NUMBER: US 60/067,341
;/ FILING DATE: 02-DEC-1997
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: JORGE A. GOLDSTEIN
;/ REGISTRATION NUMBER: 29,021
;/ REFERENCE/DOCKET NUMBER: 0977.1840002
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-371-2600
;/ TELEFAX: 202-371-2540
;/ INFORMATION FOR SEQ ID NO: 6:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 241 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;/ US-09-791-540-6
;/
;/ Query Match 91.0%; Score 539; DB 9; Length 241;
;/ Best Local Similarity 89.4%; Pred. No. 7.4e-41;
;/ Matches 101; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
;/
;/ Qy 1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLYSQKKNYLAWYQKQSPKLLIYWASAR 60
;/ Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLYSQKKNYLAWYQKQSPKLLIYWASAR 60
;/
;/ Qy 61 ESGVPRFSGSGSDTFTLTISVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
;/ Db 61 ESGVPRFTGSGSDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113
;/
;/ RESULT 25
;/ US-10-915-069-6
;/ Sequence 6, Application US/10915069
;/ Publication No. US20050008650A1
;/ GENERAL INFORMATION:
;/ APPLICANT: WHITLOW, MARC
;/ SHORR, ROBERT G.L.
;/ FILPULA, DAVID R.
;/ LEE, LIHSYNG S.
;/ TITLE OF INVENTION: POLYALKYLENE OXIDE-MODIFIED SINGLE CHAIN
;/ NUMBER OF SEQUENCES: 6
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;/ STREET: 1100 NEW YORK AVENUE, SUITE 600
;/ CITY: WASHINGTON
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.30

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:37:36 ; Search time 29.869 Seconds
(without alignments)
284.911 Million cell updates/sec

Title: US-10-058-069-9_COPY_21_134

Perfect score: 592

Sequence: 1 DIVWSQSPDSLAISLGRVT.....QQYISYPLTGTGAKLELKR 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents: AA-
1: /cgm2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	587	99.2	113	4	US-08-961-309-73
2	587	99.2	113	4	US-09-830-748B-13
3	550	92.9	113	5	PCT-US93-08435-6
4	545	92.1	113	5	PCT-US93-08435-8
5	541	91.4	134	4	US-08-961-309-58
6	540	91.2	113	2	US-08-263-911-2
7	540	91.2	113	2	US-08-819-033-1
8	540	91.2	113	3	US-09-025-203-7
9	540	91.2	113	3	US-09-025-203-13
10	540	91.2	113	4	US-08-961-309-71
11	540	91.2	113	4	US-09-999-021-7
12	540	91.2	113	4	US-09-999-021-13
13	540	91.2	113	4	US-09-999-025-7
14	540	91.2	113	4	US-09-999-025-13
15	540	91.2	113	4	US-10-040-997-7
16	540	91.2	113	4	US-10-040-997-13
17	540	91.2	113	4	US-09-999-040-7
18	540	91.2	113	4	US-09-999-040-13
19	540	91.2	113	4	US-09-998-817-7
20	540	91.2	113	4	US-09-998-817-13
21	540	91.2	133	2	US-08-822-028-12
22	540	91.2	133	3	US-08-479-285-12
23	540	91.2	133	4	US-08-503-653A-12
24	540	91.2	275	3	US-08-463-903-8
25	540	91.2	275	3	US-08-463-903-17
26	540	91.2	275	3	US-07-935-695-8
27	540	91.2	275	3	US-07-935-695-17


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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08435
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,654
/ FILING DATE: 09-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: SBC P50107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 540-9200
/ TELEFAX: (215) 540-5818
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US93-08435-6

Query Match 92.9%; Score 550; DB 5; Length 113;
Best Local Similarity 91.2%; Pred. No. 1.2e-44;
Matches 103; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIVMSQPSDLSVSLGERVTLNCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 1 DIVMTQPSDLSVSLGERATINCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASTR 60
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFSGSGSGTDFTLTISSLQAEADVAVVYCCQYYSYPRTFGGTKVEIK 113

RESULT 4
PCT-US93-08435-8
/ Sequence 8, Application PC/TUS9308435
/ GENERAL INFORMATION:
/ APPLICANT: SmithKline Beecham, Corporation
/ APPLICANT: U. S. Government, Secretary of
/ APPLICANT: the Navy
/ APPLICANT: U. S. Government, Secretary of
/ APPLICANT: the Army
/ TITLE OF INVENTION: Novel Antibodies for Conferring Passive
/ TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Howson and Howson
/ STREET: Box 457, 321 Norristown Road
/ CITY: Spring House
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19477
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/08435
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,654
/ FILING DATE: 09-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
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/ REFERENCE/DOCKET NUMBER: SBC P50107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 540-9200
/ TELEFAX: (215) 540-5818
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US93-08435-8

Query Match 92.1%; Score 545; DB 5; Length 113;
Best Local Similarity 90.3%; Pred. No. 3.6e-44;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIVMSQPSDLSVSLGERVTLNCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 1 DIVMTQPSDLSVSLGERATINCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASTR 60
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFSGSGSGTDFTLTISSLQAEADVAVVYCCQYYSYPRTFGGTKVEIK 113

RESULT 5
US-08-961-309-58
/ Sequence 58, Application US/08961309
/ Patent No. 6495137
/ GENERAL INFORMATION:
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Richard, Ruth A.
/ APPLICANT: Johnson, Kimberly S.
/ APPLICANT: Schlom, Jeffrey
/ APPLICANT: Kashmiri, Syed V.S.
/ APPLICANT: Shu, Liming
/ APPLICANT: Padian, Eduardo A.
/ TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
/ TITLE OF INVENTION: Capable of Binding to TAG-72
/ FILE REFERENCE: 37777E
/ CURRENT APPLICATION NUMBER: US/08/961,309
/ CURRENT FILING DATE: 1997-10-30
/ EARLIER APPLICATION NUMBER: US 60/030,173
/ EARLIER FILING DATE: 1996-10-31
/ EARLIER APPLICATION NUMBER: US 08/261,354
/ EARLIER FILING DATE: 1994-06-16
/ EARLIER APPLICATION NUMBER: US 07/964,536
/ EARLIER FILING DATE: 1992-10-20
/ EARLIER APPLICATION NUMBER: US 07/510,697
/ EARLIER FILING DATE: 1990-07-17
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: Microsoft Word 97 SR-2
/ SEQ ID NO 58
/ LENGTH: 134
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Hum4 VL
/ LOCATION: 1..134
/ US-08-961-309-58

Query Match 91.4%; Score 541; DB 4; Length 134;
Best Local Similarity 88.6%; Pred. No. 1e-43;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIVMSQPSDLSVSLGERVTLNCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASAR 60
Db 21 DIVMTQPSDLSVSLGERATINCKSSQSLSYGNQKNYLAWYQKQSPKLLIYWASTR 80
QY 61 ESGVPRFSGSGSGTDFTLTISSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 114
Db 81 ESGVPRFSGSGSGTDFTLTISSLQAEADVAVVYCCQYYSYPLTFGGTKVIR 134
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RESULT 6
US-08-263-911-2
; Sequence 2, Application US/08263911
; Patent No. 5877291
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S
; APPLICANT: Gourlie, Brian B
; TITLE OF INVENTION: MULTIVALENT SINGLE CHAIN ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Duane C. Ulmer
; STREET: P.O. Box 1967
; CITY: Midland
; STATE: MI
; COUNTRY: US
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/263,911
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,263
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ulmer, Duane C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-41,014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-263-911-2

Query Match          91.2%; Score 540; DB 2; Length 113;
Best Local Similarity 90.3%; Pred.No. 1.le-43; Indels 0; Gaps 0;
Matches 102; Conservative 7; Mismatches 4;

Qy      1 DIVMSGPDSLAVSLGSRVLTINCKSSQSLLYSGNQKNYLAWYQKPGSQPKLIYWASAR 60
        |||||
Db      1 DIVMSGPSPLSVSGEKVTLSCKSSQLLYSGNQKNYLAWYQKPGSQPKLIYWASAR 60
        |||||

Qy      61 ESGVPDRFSGSGGTDTFTLTISSVQAEADVAVYYCQQIYSYPLTFGAGTKLELK 113
        |||||
Db      61 ESGVPDRFTGSGGTDTFTLTISSVKTEDLAVYYCQQIYSYPLTFGAGTKLVK 113
        |||||

RESULT 7
US-08-819-033-1
; Sequence 1, Application US/08819033
; Patent No. 5917021
; GENERAL INFORMATION:
; APPLICANT: LEE, LIHSYNG STANFORD
; TITLE OF INVENTION: STABILIZED MONOMERIC PROTEIN
; MEDIUM TYPE: COMPOSITIONS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGGTDTLTLSISSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFTGSGGTDTLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 9

US-09-025-203-13
; Sequence 13, Application US/09025203
; Patent No. 6348581
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/025,203
; CURRENT FILING DATE: 1998-02-18
; EARLIER APPLICATION NUMBER: PCT US97/19641
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 60/030,173
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-09-025-203-13

Query Match 91.2%; Score 540; DB 3; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.le-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGGTDTLTLSISSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFTGSGGTDTLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 10

US-08-961-309-71
; Sequence 71, Application US/08961309
; Patent No. 6495137
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Johnson, Kimberly S.
; APPLICANT: Schlom, Jeffrey S.
; APPLICANT: Kashmiri, Syed V.S.
; APPLICANT: Shu, Liming
; APPLICANT: Padlan, Eduardo A.
; TITLE OF INVENTION: Composite Antibodies of Humanized Human Subgroup IV Light Chain
; FILE REFERENCE: 3777E
; CURRENT APPLICATION NUMBER: US/08/961,309
; CURRENT FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 60/030,173
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 08/261,354
; EARLIER FILING DATE: 1994-06-16
; EARLIER APPLICATION NUMBER: US 07/964,536

; EARLIER FILING DATE: 1992-10-20
; EARLIER APPLICATION NUMBER: US 07/510,697
; EARLIER FILING DATE: 1990-07-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 71
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
US-08-961-309-71

Query Match 91.2%; Score 540; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.le-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGGTDTLTLSISSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFTGSGGTDTLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 11

US-09-999-021-7
; Sequence 7, Application US/09999021
; Patent No. 6737060
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VK
; LOCATION: 1..113
US-09-999-021-7

Query Match 91.2%; Score 540; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.le-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
Db 1 DIVMSQSPSLPVSVEKVTLSCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGGTDTLTLSISSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPRFTGSGGTDTLTLSISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 12

US-09-999-021-13

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; Sequence 13, Application US/09999021
; Patent No. 6737060
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,021
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
; US-09-999-021-13

Query Match          91.2%; Score 540; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.1e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db      1 DIVMSQSPSPLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60

QY      61 ESGVPRFRSGSGTGDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
Db      61 ESGVPRFRFTGSGSGTGDTFTLTSSVKTEDLAVYCCQYYSYPLTFGAGTKLVLK 113

RESULT 14
US-09-999-025-13
; Sequence 13, Application US/09999025
; Patent No. 6737061
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,025
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 13
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VL
; LOCATION: 1..113
; US-09-999-025-13

Query Match          91.2%; Score 540; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.1e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db      1 DIVMSQSPSPLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60

QY      61 ESGVPRFRSGSGTGDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
Db      61 ESGVPRFRFTGSGSGTGDTFTLTSSVKTEDLAVYCCQYYSYPLTFGAGTKLVLK 113

RESULT 13
US-09-999-025-7
; Sequence 7, Application US/09999025
; Patent No. 6737061
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/999,025
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: PCT US97/19641
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 60/030,173
; PRIOR FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Word 97 SR-2
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: Murine CC49 VK
; LOCATION: 1..113
; US-09-999-025-7

Query Match          91.2%; Score 540; DB 4; Length 113;
Best Local Similarity 90.3%; Pred. No. 1.1e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      1 DIVMSQSPDLSAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db      1 DIVMSQSPSPLPVSVGEKVTLSCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60

QY      61 ESGVPRFRSGSGTGDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELK 113
Db      61 ESGVPRFRFTGSGSGTGDTFTLTSSVKTEDLAVYCCQYYSYPLTFGAGTKLVLK 113

RESULT 15
US-10-040-997-7
; Sequence 7, Application US/10040997
; Patent No. 6752990
; GENERAL INFORMATION:
; APPLICANT: Anderson, W.H. Kerr
; APPLICANT: Tempest, Philip R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Harris, William J.
; APPLICANT: Armour, Kathryn
; TITLE OF INVENTION: High Affinity Humanized Anti-TAG-72 Monoclonal Antibodies
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/040,997
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 09/025,203
; PRIOR FILING DATE: 1998-02-18
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; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-822-028-12

Query Match          91.2%; Score 540; DB 2; Length 133;
Best Local Similarity 90.3%; Pred. No. 1.3e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 60
Db 21 DIVMSQSPSLPVSVEKVTLSCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 80
Qy 61 ESGVPRFSGSGGTDFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
Db 81 ESGVPRFTGSGGTDFTLTISVSKTEDLAVYCCQYYSYPLTFGAGTKLVK 133

RESULT 22
US-08-479-285-12
; Sequence 12, Application US/08479285
; Patent No. 6207815
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
; TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUANE C ULMER
; STREET: P.O. BOX 1967
; CITY: MIDLAND
; STATE: MICHIGAN
; COUNTRY: USA
; ZIP: 48641-1967
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,285
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/040687
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ULMER, DUANE C
; REGISTRATION NUMBER: 34,941
; REFERENCE/DOCKET NUMBER: C-37, 075C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 636-8104
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-285-12

Query Match          91.2%; Score 540; DB 3; Length 133;
Best Local Similarity 90.3%; Pred. No. 1.3e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 60
Db 21 DIVMSQSPSLPVSVEKVTLSCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 80
Qy 61 ESGVPRFSGSGGTDFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
Db 81 ESGVPRFTGSGGTDFTLTISVSKTEDLAVYCCQYYSYPLTFGAGTKLVK 133

RESULT 23
US-09-503-653A-12
; Sequence 12, Application US/09503653A
; Patent No. 6641999
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S
; APPLICANT: GOURLIE, BRIAN B
; APPLICANT: RIXON, MARK W
; APPLICANT: ANDERSON, WH KERR
; APPLICANT: KAPLAN, DONALD A
; APPLICANT: SCHLOM, JEFFREY
; TITLE OF INVENTION: Probing Method for Identifying Antibodies
; TITLE OF INVENTION: Specific for Selected Antigens
; FILE REFERENCE: 37075H-CIP1
; CURRENT APPLICATION NUMBER: US/09/503,653A
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 08/040,687
; PRIOR FILING DATE: 1993-03-31
; PRIOR APPLICATION NUMBER: US 07/424,362
; PRIOR FILING DATE: 1989-10-19
; PRIOR APPLICATION NUMBER: US 07/261,942
; PRIOR FILING DATE: 1988-10-24
; PRIOR APPLICATION NUMBER: US 07/259,943
; PRIOR FILING DATE: 1988-10-19
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: MICROSOFT Word 97 SR-2
; SEQ ID NO 12
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; NAME/KEY: CHAIN
; LOCATION: 1..113
US-09-503-653A-12

Query Match          91.2%; Score 540; DB 4; Length 133;
Best Local Similarity 90.3%; Pred. No. 1.3e-43;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 60
Db 21 DIVMSQSPSLPVSVEKVTLSCKSSQSLYSNGKNYLAAYQKPGQSPKLLIYWASAR 80
Qy 61 ESGVPRFSGSGGTDFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
Db 81 ESGVPRFTGSGGTDFTLTISVSKTEDLAVYCCQYYSYPLTFGAGTKLVK 133

RESULT 24
US-08-463-903-8
; Sequence 8, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: MEZES, PETER S.
; APPLICANT: RICHARD, RUTH A.
; APPLICANT: AFFHOLTER, JOSEPH A.
; APPLICANT: KOTITE, NICOLAS J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; FILE REFERENCE: 40224A US
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05
; EARLIER APPLICATION NUMBER: US 07/935,695
```

Search completed: July 25, 2005, 08:12:50
Job time : 29.869 secs

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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:32:04 ; Search time 120.969 Seconds
(without alignments)
364.478 Million cell updates/sec

Title: US-10-058-069-9_COPY_21_134

Perfect score: 500.000

Sequence: 1 DIVNSQSPSLAVSLGERTV.....QQYYSYPLTFGAGTKLELKR 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	100.0	137	3	AAY95243 Humanised
2	592	100.0	240	5	AEE27927 Human CC4
3	592	100.0	240	6	ABB82836 Antibody
4	587	99.2	113	6	ADB17745 Humanised
5	587	99.2	113	7	ADG46865 Humanised
6	587	99.2	113	6	ADB17751 Humanised
7	587	99.2	133	7	ADG46872 Humanised
8	550	92.9	113	2	AAR50313 Humanised
9	545	92.1	113	2	AAR50314 Humanised
10	541	91.4	134	2	AAY50690 Human Hum
11	541	91.4	134	6	ADB17730 Human Hum
12	541	91.4	134	7	ADG46850 Human Hum
13	541	91.4	259	7	ADG32322 Mouse scf
14	541	91.4	329	7	ADG32359 Precursor
15	540	91.2	113	2	AAR56964 CC49 V-11
16	540	91.2	113	2	AAY42267 Murine an
17	540	91.2	113	2	AAY97177 Monoclonal
18	540	91.2	113	2	AAY05759 Anti-TAG
19	540	91.2	113	5	AAR78320 Murine CC
20	540	91.2	113	6	ABU09371 Light cha
21	540	91.2	113	6	ABU09365 Murine mo
22	540	91.2	113	6	ABU10146 Murine TA
23	540	91.2	113	6	ABU10140 Murine TA
24	540	91.2	113	6	ADB17743 Native CC
25	540	91.2	113	6	ABU62757 Murine mo

26	540	91.2	113	6	ABU62763	Abu62763 Murine mo
27	540	91.2	113	7	AAE39069	Aae39069 Murine CC
28	540	91.2	113	7	AAE39063	Aae39063 Murine CC
29	540	91.2	113	7	ADG46863	Adg46863 Murine CC
30	540	91.2	113	8	ADP71406	Adp71406 Mouse CC4
31	540	91.2	113	3	AAY57051	Aay57051 Anino aci
32	540	91.2	113	3	AAY90719	Aay90719 CC49 VL r
33	540	91.2	133	4	AAU02138	Aau02138 Mouse par
34	540	91.2	133	7	ADK66824	Adk66824 Mouse CC4
35	540	91.2	242	4	AAAB31422	Aab31422 Protein u
36	540	91.2	262	4	AAAB31421	Aab31421 Protein u
37	540	91.2	271	4	AAAB31423	Aab31423 Protein u
38	540	91.2	272	4	AAAB31424	Aab31424 Protein u
39	540	91.2	444	6	ABJ39018	Abj39018 CC49 sing
40	540	91.2	553	2	AAR56966	Aar56966 CC49 VL-L
41	540	91.2	553	2	AAR56967	Aar56967 CC49 VL-L
42	540	91.2	553	2	AAW97181	Aaw97181 A multiva
43	540	91.2	553	2	AAW97180	Aaw97180 A multiva
44	540	91.2	553	2	AAW05762	Aay05762 CC49 sing
45	540	91.2	553	2	AAW05763	Aay05763 CC49 sing
46	539	91.0	240	2	AAW50161	Aay50161 Human res
47	539	91.0	242	2	AAW55865	Aar55865 CC49 VL/
48	539	91.0	242	2	AAW95439	Aaw95439 Linked fu
49	539	91.0	242	2	AAW88101	Aaw88101 Single ch
50	539	91.0	242	3	AAW07937	Aab07937 A single-
51	539	91.0	242	3	AAW57256	Aay57256 4-4-20 Vh
52	539	91.0	242	3	AAW27681	Aab27681 Bivalent
53	539	91.0	242	3	AAW80926	Aay80926 Single ch
54	539	91.0	242	3	AAW54835	Aay54835 Antibody
55	539	91.0	242	6	ABU61811	Abu61811 Antigen b
56	539	91.0	244	2	AAW88096	Aaw88096 Single-ch
57	539	91.0	244	3	AAW07932	Aab07932 A heterob
58	539	91.0	244	3	AAW57251	Aay57251 4-4-20 Vh
59	539	91.0	244	3	AAW27676	Aab27676 Bivalent
60	539	91.0	244	3	AAW80921	Aay80921 Single ch
61	539	91.0	244	6	ABU61806	Abu61806 Antigen b
62	539	91.0	248	2	AAW37646	Aar37646 Sequence
63	539	91.0	248	2	AAW97382	Aar97382 CC49 VL-P
64	539	91.0	249	2	AAW97888	Aaw97888 CC49/218
65	539	91.0	257	5	AAW81524	Aaw81524 Single ch
66	539	91.0	257	5	AAU75157	Aau75157 CC49/218
67	539	91.0	257	6	ABG73145	Abg73145 CC49/218
68	539	91.0	257	6	ABG73865	Abg73865 CC49/218
69	539	91.0	262	2	AAW97380	Aar97380 CC49/212
70	539	91.0	264	2	AAW97381	Aar97381 PLAP CC49
71	539	91.0	269	5	AAU75158	Aau75158 CC49/218
72	539	91.0	269	6	ABG73146	Abg73146 CC49/218
73	539	91.0	269	6	ABG73866	Abg73866 CC49/218
74	539	91.0	432	5	AAO17498	Aao17498 Antibody-
75	539	91.0	480	5	AAO17495	Aao17495 Antibody-
76	539	91.0	483	2	AAW88099	Aaw88099 A protei
77	539	91.0	483	3	AAW07935	Aab07935 A divalen
78	539	91.0	483	3	AAW57254	Aay57254 Divalent
79	539	91.0	483	3	AAW27679	Aab27679 Bivalent
80	539	91.0	483	3	AAW80924	Aay80924 Bivalent
81	539	91.0	483	6	ABU61809	Abu61809 Divalent
82	539	91.0	486	2	AAW37649	Aar37649 Sequence
83	539	91.0	601	5	AAW49760	Aam49760 TNF-selec
84	539	91.0	614	5	AAO17494	Aao17494 Antibody-
85	539	91.0	658	5	AAW49759	Aam49759 TNF-selec
86	538	90.9	113	2	AAW50145	Aay50145 Antibody
87	538	90.9	113	6	ABW898749	Abb898749 Human res
88	536	90.5	120	4	AAW65565	Aaw65565 Anino aci
89	536	90.5	161	7	ADG46871	Adg46871 Protein e
90	536	90.5	171	2	AAW38320	Aar38320 Sequence
91	536	90.5	171	2	AAW50693	Aay50693 Plaemid p
92	536	90.5	171	2	AAW57184	Aay57184 Amino aci
93	536	90.5	274	2	AAW38319	Aar38319 Sequence
94	536	90.5	274	2	AAW50692	Aay50692 Human Hum
95	536	90.5	274	2	AAW57183	Aay57183 Amino aci
96	536	90.5	274	6	ADB17738	Adb17738 Hum4 VL-C
97	536	90.5	274	6	ADG46858	Adg46858 Hum4VL-11
98	536	90.5	284	2	AAW38321	Aar38321 Sequence


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SQ Sequence 240 AA;
Query Match 100.0%; Score 592; DB 5; Length 240;
Best Local Similarity 100.0%; Pred. No. 7.4e-41;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIWMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNQKNYLAWYQKQSPKLIYASAR 60
    |||
DB 21 DIWMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNQKNYLAWYQKQSPKLIYASAR 80
    |||
OY 61 ESGVPRFSGSGSDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKR 114
    |||
DB 81 ESGVPRFSGSGSDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKR 134

RESULT 3
ADB17745
ID ABB82836 standard; protein; 240 AA.
XX
AC ABB82836;
XX
DT 31-MAR-2003 (first entry)
XX
DE Antibody huCC49 light chain.
XX
KW CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vesotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thymimetic; hepatotropic; haemostatic; antileptotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antinflammatory.
XX
OS Homo sapiens.
XX
PN WO200296948-A2.
XX
PD 05-DEC-2002.
XX
PF 29-JAN-2002; 2002WO-US0002374.
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
PR 21-DEC-2001; 2001US-0341858P.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Braslowsky GR, Hanna N, Chinn P, Hariharan K;
XX
DR WPI; 2003-140446/13.
XX
DR N-PSDB; ABZ24020.
XX
PT Novel dimeric antibody useful for treating immune disorder and neoplastic
PT disorder, has several non-covalently associated monomeric subunits.
XX
PS Example 1; Fig 5A; 78pp; English.
XX
CC The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody huCC49 light chain
XX
SQ Sequence 240 AA;
Query Match 99.2%; Score 587; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.3e-41;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DIWMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNQKNYLAWYQKQSPKLIYASAR 60
    |||
DB 21 DIWMSQSPDSLAVSLGERTVLNCKSSQSLLYSGNQKNYLAWYQKQSPKLIYASAR 80
    |||
OY 61 ESGVPRFSGSGSDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKR 114
    |||
DB 81 ESGVPRFSGSGSDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLELKR 134

RESULT 4
ADB17745
ID ADB17745 standard; protein; 113 AA.
XX
AC ADB17745;
XX
DT 20-NOV-2003 (first entry)
XX
DE Humanised CC49 light chain variable region fragment.
XX
KW anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAMA; accelerated whole body clearance; human; mouse.
XX
OS Mus musculus.
XX
OS Homo sapiens.
XX
PN US6495137-B1.
XX
PD 17-DEC-2002.
XX
PF 30-OCT-1997; 97US-00961309.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-615251/58.
XX
PT New composite and humanized anti-tumor-associated glycoprotein-72
PT monoclonal antibody useful for detecting or treating cancer.
XX
PS Claim 3; Fig 32A; 130pp; English.
XX
CC The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (TAG-72) antibody or its fragment comprising a
CC complementarity determining region (CDR)-grafted light chain having light
CC chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
CC IV kappa light chain. The composition is suitable for the treatment and
CC detection of cancer. The novel antibody has the ability to bind
CC specifically to malignant cells and does not bind to normal cells. It
CC greatly minimises or eliminates harmful hypersensitivity anti-mouse
CC antibody (HAMA) responses. The relatively small size and human character
CC of the composite Hum4V-L, V-H single chain antibodies accelerate whole
CC body clearance, thus reducing the waiting period after injection before
CC surgery is initiated. The present sequence represents the amino acid
CC sequence of the humanised CC49 light chain variable region fragment.
XX
SQ Sequence 113 AA;
Query Match 99.2%; Score 587; DB 6; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.3e-41;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGSPKLLIYWASAR 60
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
RESULT 5
ADG46865
ID ADG46865 standard; protein; 113 AA.
XX
AC ADG46865;
XX
DT 11-MAR-2004 (first entry)
XX
DE Humanised CC49 VL protein fragment with Hum4 VL framework regions.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; mouse; human; chimeric.
XX
OS Chimeric.
OS Unidentified.
OS Mus musculus.
OS Homo sapiens.
XX
XX
FH Key
FT Location/Qualifiers
FT 1..23
FT Region /note= "Human LEN light chain variable region FR1"
FT Region 24..40
FT Region /note= "Murine CC49 light chain variable region CDR1"
FT Region 41..55
FT Region /note= "Human LEN light chain variable region FR2"
FT Region 56..62
FT Region /note= "Murine CC49 light chain variable region CDR2"
FT Region 63..94
FT Region /note= "Human LEN light chain variable region FR3"
FT Region 95..103
FT Region /note= "Murine CC49 light chain variable region CDR3"
FT Region 104..113
FT Region /note= "Human LEN light chain variable region FR4"
XX
PN US2003165498-A1.
XX
XX
PD 04-SEP-2003.
XX
XX
PF 25-SEP-2002; 2002US-00255478.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97US-00961309.
XX
XX
PA (MEZE/) MEZES P S.
PA (RICH/) RICHARD R A.
PA (JOHN/) JOHNSON K S.
PA (SCHL/) SCHLOM J.
PA (KASH/) KASHMIRI S V S.
PA (SHUL/) SHU L.
PA (PADL/) PADLAN E A.
XX
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-898033/82.
XX
XX New humanized or composite anti-TAG-72 monoclonal antibody with subgroup
PT IV kappa light chain framework regions, useful in the fields of

PT immunology and genetic engineering, particularly for detecting and/or
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 73; 133pp; English.
XX
CC The invention relates to a humanised or composite anti-tumour-associated
glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody
comprises a complementarity determining region (CDR)-grafted light chain
CC having non-human CDRs grafted to a human subgroup IV kappa light chain.
CC The invention is useful in gene-therapy. The methods and compositions of
CC the present invention are useful in the fields of immunology and genetic
CC engineering, particularly for detecting and/or treating cancer. The
CC present sequence is humanised CC49 VL protein fragment with Hum4 VL
CC framework regions used in the exemplification of the invention.
XX
SQ Sequence 113 AA;
Query Match 99.2%; Score 587; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.3e-41;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGSPKLLIYWASAR 60
DB 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGSPKLLIYWASAR 60
QY 61 ESGVDPDRFSGSGGTDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
DB 61 ESGVDPDRFSGSGGTDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
RESULT 6
ADBI7751
ID ADBI7751 standard; protein; 133 AA.
XX
AC ADBI7751;
XX
DT 20-NOV-2003 (first entry)
XX
DE Humanised CC49 light chain variable region.
XX
KW anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAMA; accelerated whole body clearance; human; mouse.
XX
OS Mus musculus.
OS Homo sapiens.
XX
PN US6495137-B1.
XX
PD 17-DEC-2002.
XX
PF 30-OCT-1997; 97US-00961309.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
XX
XX (DOMC) DOW CHEM CO.
PA
XX Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-615251/58.
DR N-PSDB; ADBI7749.
XX
XX New composite and humanized anti-tumor-associated glycoprotein-72
PT monoclonal antibody useful for detecting or treating cancer.
XX
XX Disclosure; Col 111-112; 130pp; English.
XX
XX The invention relates to a humanised or composite anti-tumour-associated

CC glycoprotein-72 (TAG-72) antibody or its fragment comprising a
CC complementarity determining region (CDR)-grafted light chain having light
CC chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
CC IV kappa light chain. The composition is suitable for the treatment and
CC detection of cancer. The novel antibody has the ability to bind
CC specifically to malignant cells and does not bind to normal cells. It
CC greatly minimises or eliminates harmful hypersensitivity anti-mouse
CC antibody (HAMA) responses. The relatively small size and human character
CC of the composite Hum4V-L, V-H single chain antibodies accelerate whole
CC body clearance, thus reducing the waiting period after injection before
CC surgery is initiated. The present sequence represents the amino acid
CC sequence of the humanised CC49 light chain variable region.
XX
XX Sequence 133 AA;
SQ
Query Match 99.2%; Score 587; DB 6; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMSQSPDLSAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
DB 21 DIVMSQSPDLSAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
QY 61 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
DB 81 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 133
RESULT 7
ADG46872
ID ADG46872 standard; protein; 133 AA.
XX
AC ADG46872;
XX
AC AC
XX
DT 11-MAR-2004 (first entry)
XX
DE Humanised CC49 VL protein with Hum4 VL framework regions.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; mouse; human; fusion protein.
XX
OS Chimeric.
OS Unidentified.
OS Mus musculus.
OS Homo sapiens.
XX
PN US2003165498-A1.
XX
PD 04-SEP-2003.
XX
PF 25-SEP-2002; 2002US-00255478.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97US-00961309.
XX
XX (MEZE/) MEZES P S.
PA (RICH/) RICHARD R A.
PA (JOHN/) JOHNSON K S.
PA (SCHL/) SCHLOM J.
PA (KASH/) KASHMIRI S V S.
PA (SHUL/) SHU L.
PA (PADL/) PADLAN E A.
XX
PI Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
XX WPI; 2003-898033/82.
DR N-PSDB; ADG46870.

XX New humanized or composite anti-TAG-72 monoclonal antibody with subgroup
PT IV kappa light chain framework regions, useful in the fields of
PT immunology and genetic engineering, particularly for detecting and/or
PT treating cancer.
XX
XX Disclosure; SEQ ID NO 80; 133pp; English.
XX
XX The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody
CC comprises a complementarity determining region (CDR)-grafted light chain
CC having non-human CDRs grafted to a human subgroup IV kappa light chain.
CC The invention is useful in gene-therapy. The methods and compositions of
CC the present invention are useful in the fields of immunology and genetic
CC engineering, particularly for detecting and/or treating cancer. The
CC present sequence is humanised CC49 VL protein with Hum4 VL framework
CC regions used in the exemplification of the invention.
XX
XX Sequence 133 AA;
SQ
Query Match 99.2%; Score 587; DB 7; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e-40;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIVMSQSPDLSAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
DB 21 DIVMSQSPDLSAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
QY 61 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 113
DB 81 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVYCCQYYSYPLTFGAGTKLELK 133
RESULT 8
AAR50313
ID AAR50313 standard; protein; 113 AA.
XX
AC AAR50313;
XX
DT 25-MAR-2003 (revised)
DT 05-OCT-1994 (first entry)
XX
DE Humanised light chain variable region Pfhlzcl-1.
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein; murine; variable;
KW light; heavy; chain; malaria.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..40
FT /label= CDR1
FT Region 56..62
FT /label= CDR2
FT Region 95..103
FT /label= CDR3
XX
PN WO9405690-A1.
XX
PD 17-MAR-1994.
XX
PF 08-SEP-1993; 93WO-US008435.
XX
PR 09-SEP-1992; 92US-00941654.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (USNA) US SEC OF NAVY.
PA (USSA) US SEC OF ARMY.
XX
PI Gross MS, Rosenberg M, Sadoff JC, Hoffman S, Sylvester DR;
PI Charoenvit Y, Hurlie M;
XX

CC therapeutic agents e.g. a radionuclide, drug, biological response
CC modifier, toxin or another antibody for the treatment of cancers. The
CC humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC hypersensitivity reactions

CC Sequence 134 AA;
Query Match 91.4%; Score 541; DB 2; Length 134;
Best Local Similarity 88.6%; Pred. No. 6.5e-37;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIVMSQPSDLSAVSLGERVTLNCKSSQSLYSNKNYLAWSQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLYSNKNYLAWSQKPGQSPKLLIYWASTR 80
OY 61 ESGVDPFRFGSGSGTDFTLTISVQAEADVAVVYCCQYYSYPLTFGGATKLELR 114
Db 81 ESGVDPFRFGSGSGTDFTLTISVQAEADVAVVYCCQYYSYPLTFGGTKVVKR 134

RESULT 11
ADBI17730
ID ADBI17730 standard; protein; 134 AA.
XX
AC ADBI17730;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human Hum4 light chain variable region.
XX
DE anti-tumour-associated glycoprotein-72; TAG-72; antibody;
KW complementarity determining region; CDR; cancer;
KW malignant cell specific binding; hypersensitivity anti-mouse antibody;
KW HAMA; accelerated whole body clearance; human.
XX
OS Homo sapiens.
XX
PN US6495137-B1.
XX
PD 17-DEC-2002.
XX
PF 30-OCT-1997; 97US-00961309.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
XX
PA (DOWC) DOW CHEM CO.
XX
PI Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
WPI: 2003-615251/58.
DR N-PSDB; ADBI17729.
XX
New composite and humanized anti-tumor-associated glycoprotein-72
PT monoclonal antibody useful for detecting or treating cancer.
XX
Example 1; Fig 10; 130pp; English.
XX
The invention relates to a humanised or composite anti-tumour-associated
CC glycoprotein-72 (TAG-72) antibody or its fragment comprising a
CC complementarity determining region (CDR)-grafted light chain having light
CC chain CDRs of a murine anti-TAG-72 antibody grafted onto a human subgroup
CC IV kappa light chain. The composition is suitable for the treatment and
CC detection of cancer. The novel antibody has the ability to bind
CC specifically to malignant cells and does not bind to normal cells. It
CC greatly minimises or eliminates harmful hypersensitivity anti-mouse
CC antibody (HAMA) responses. The relatively small size and human character
CC of the composite Hum4V-L, V-H single chain antibodies accelerate whole
CC body clearance, thus reducing the waiting period after injection before
CC surgery is initiated. The present sequence represents the amino acid

CC sequence of the human Hum4 light chain variable region.
XX
SQ Sequence 134 AA;
Query Match 91.4%; Score 541; DB 6; Length 134;
Best Local Similarity 88.6%; Pred. No. 6.5e-37;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIVMSQPSDLSAVSLGERVTLNCKSSQSLYSNKNYLAWSQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLYSNKNYLAWSQKPGQSPKLLIYWASTR 80
OY 61 ESGVDPFRFGSGSGTDFTLTISVQAEADVAVVYCCQYYSYPLTFGGATKLELR 114
Db 81 ESGVDPFRFGSGSGTDFTLTISVQAEADVAVVYCCQYYSYPLTFGGTKVVKR 134

RESULT 12
ADG46850
ID ADG46850 standard; protein; 134 AA.
XX
AC ADG46850;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human Hum4VL protein.
XX
KW Anti-tumour-associated glycoprotein-72; anti-TAG-72 antibody;
KW complementarity determining region; CDR-grafted light chain;
KW subgroup IV kappa light chain; gene-therapy; immunology;
KW genetic engineering; cancer; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 18 /note= "Encoded by CCC"
FT Region 44..60 /note= "Complementarity determining region 1"
FT Region 76..82 /note= "Complementarity determining region 2"
FT Region 115..123 /note= "Complementarity determining region 3"
FT Misc-difference 132 /note= "Encoded by AAA"
XX
PN US2003165498-A1.
XX
PD 04-SEP-2003.
XX
PF 25-SEP-2002; 2002US-00255478.
XX
PR 19-APR-1990; 90US-00510697.
PR 20-OCT-1992; 92US-00964536.
PR 16-JUN-1994; 94US-00261354.
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97US-00961309.
XX
PA (MEZE/) MEZES P S.
PA (RICH/) RICHARD R A.
PA (JOHN/) JOHNSON K S.
PA (SCHL/) SCHLOM J.
PA (KASH/) KASHMIRI S V S.
PA (SHUL/) SHU L.
PA (PADL/) PADLAN E A.
XX
Mezes PS, Richard RA, Johnson KS, Schlom J, Kashmiri SVS, Shu L;
PI Padlan EA;
XX
WPI: 2003-898033/82.
DR N-PSDB; ADG46849.
XX
New humanized or composite anti-TAG-72 monoclonal antibody with subgroup

PT IV kappa light chain framework regions, useful in the fields of
PT immunology and genetic engineering, particularly for detecting and/or
PT treating cancer.

Disclosure; SEQ ID NO 58; 133pp; English.

The invention relates to a humanised or composite anti-tumour-associated glycoprotein-72 (anti-TAG-72) antibody or its fragment. The antibody comprises a complementarity determining region (CDR)-grafted light chain having non-human CDRs grafted to a human subgroup IV kappa light chain. The invention is useful in gene-therapy. The methods and compositions of the present invention are useful in the fields of immunology and genetic engineering, particularly for detecting and/or treating cancer. The present sequence is human Hum4V1 protein used in the exemplification of the invention.

resistant transgenic plants that are protected against fungal infection. Accordingly, a method is described for antibody based resistance in plants such that the undesirable and expensive chemical controls often used in agriculture are not required. The present invention provides antibodies, recombinant antibodies and fragments thereof, as well as fusion proteins that can be used as pathogen-specific antibodies targeted to different plant cell compartments. As such, these fungicidal agents confer a broad spectrum of disease resistance in both economically important crops and ornamental plants. This polypeptide is an antibody used in an exemplification of the invention.

CC Accordingly, a method is described for antibody based resistance in
 CC plants such that the undesirable and expensive chemical controls often
 CC used in agriculture are not required. The present invention provides
 CC antibodies, recombinant antibodies and fragments thereof, as well as
 CC fusion proteins that can be used as pathogen-specific antibodies targeted
 CC to different plant cell compartments. As such, these fungicidal agents
 CC confer a broad spectrum of disease resistance in both economically
 CC important crops and ornamental plants. This polypeptide is a precursor
 CC fusion protein of the order [AFP - linker - antibody fragment] of the
 CC invention.

XX SQ Sequence 329 AA;
 Query Match 91.4%; Score 541; DB 7; Length 329;
 Best Local Similarity 87.7%; Pred. No. 1.5e-36;
 Matches 100; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
 Db DIVLSQSPSSLVAVSGKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASTR 267
 QY 61 ESGVDPDRFSGSGDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELKR 114
 Db 268 ESGVDPDRFSGSGDTFTLTISVKAEDLAVYCCQYYSYPLTFGAGTKLEIKR 321

RESULT 15
 AAR56964
 ID AAR56964 standard; protein; 113 AA.
 XX
 AC AAR56964;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-FEB-1995 (first entry)
 XX
 XX CC49 V-light.
 XX Multivalent single chain antibody; antigen binding site; diagnosis;
 KW peptide linker; variable; light; heavy; VL; VH; CC antibody;
 KW tumour-associated glycoprotein 72 antigen; TAG-72.
 XX
 OS Mus musculus.
 XX
 PN WO9413806-A1.
 XX
 PD 23-JUN-1994.
 XX
 PF 10-DEC-1993; 93WO-US012039.
 XX
 PR 11-DEC-1992; 92US-00990263.
 XX
 XX (DOWC) DOW CHEM CO.
 XX
 XX Mezes PS, Gourlie BB;
 XX
 DR WPI; 1994-217882/26.
 DR N-PSDB; AAO68657.
 XX
 PT Multivalent single chain antibodies with two or more active antigen
 PT binding sites are used for use in diagnosis and therapeutics, reaching
 PT their target tissue more rapidly and are cleared more quickly from the
 PT body.

XX
 PS Claim 3; Fig 3; 48pp; English.
 XX
 XX Multivalent single chain antibodies are formed by using a peptide linker
 CC to covalently link two or more single chain antibodies, each single chain
 CC antibody having a variable light (VL) domain linked to a variable heavy
 CC (VH) chain domain by a peptide linker. The VL and VH domains are pref.
 CC obtained from a series of CC antibodies against tumour-associated
 CC glycoprotein 72 antigen (TAG-72), eg. see AAO68657 for VL of CC49 and
 CC AAO68658 for VH of CC49. The linker is pref. based on the helical linker
 CC designated 205C, eg. see AAR56963. Two plasmids were constructed to

CC produce multivalent single chain antibodies. The sequences of p49LHLH and
 CC p49LHLH are given in AAO68659-60. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 113 AA;

Query Match 91.2%; Score 540; DB 2; Length 113;
 Best Local Similarity 90.3%; Pred. No. 6.7e-37;
 Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
 Db 1 DIVMSQSPSSLVAVSGKVTLSCKSSQSLLYSGNQKNYLAWYQKQSPKLLIYWASAR 60
 QY 61 ESGVDPDRFSGSGDTFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELX 113
 Db 61 ESGVDPDRFSGSGDTFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 16
 AAY42267
 ID AAY42267 standard; protein; 113 AA.
 XX
 AC AAY42267;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Murine anti-TAG-72 monoclonal antibody CC49 VL region.
 DE
 KW Tumour-associated glycoprotein; TAG-72; carcinoma; cancer; tumour;
 KW antibody; therapy; immunogenic; humanise.
 XX
 OS Mus sp.
 XX
 PN WO9943816-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 25-FEB-1998; 98WO-US003679.
 XX
 PR 25-FEB-1998; 98WO-US003679.
 XX
 PA (DOWC) DOW CHEM CO.
 XX
 XX Anderson WHK, Tempest PR, Carr FU, Harris WJ, Armour K;
 XX WPI; 1999-540593/45.
 XX
 PT New humanized murine antibody specific for TAG-72 antigen, for treatment
 PT and diagnosis of cancer.
 XX
 PS Example; Fig 2; 75pp; English.

XX
 CC This sequence represents murine monoclonal antibody CC49 light chain
 CC variable region (VL). CC49 binds TAG-72 (tumour-associated glycoprotein),
 CC a human carcinoma antigen expressed by various human tumour cells.
 CC CC49 could be used as an anticancer agent; however, as it is from a
 CC foreign species, it may cause a neutralising antibody response in the
 CC patient. In addition, its constant domains are murine and it may not
 CC exhibit human effector functions. To overcome these potential problems,
 CC humanised CC49 derivative antibodies were produced. These were produced
 CC by obtaining the CC49 heavy and light chain variable sequences,
 CC identifying the complementarity determining regions (CDRs) and grafting
 CC the CDR-encoding DNA sequences onto human antibody framework DNA
 CC sequences. Such humanised antibodies can be used in cancer therapy. The
 CC antibodies can be used to treat or prevent TAG-72-expressing cancers (e.g. of
 CC breast, ovary, prostate or colon) and to detect TAG-72-expressing cells,
 CC either in vitro or in vivo (particularly by tumour imaging to identify
 CC tumours and metastases before surgery), for diagnosis or prognosis. As
 CC the humanised antibodies are not significantly immunogenic, (i.e. they do
 CC not induce a human anti-murine antibody or allergic response, or non-
 CC specific cytotoxicity) they can be administered repeatedly. They retain
 CC specificity for TAG-72, and have improved clearance (allowing efficient

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CC targeting) and metabolic properties
XX
SQ Sequence 113 AA;

Query Match          91.2%; Score 540; DB 2; Length 113;
Best Local Similarity 90.3%; Pred. No. 6.7e-37;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDLSAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIVMSQSPSLPVSIVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ESGVDPDRFSGSGGTDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ESGVDPDRFSGSGGTDTFTLTSSVKTEDLAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 17
AAW97177
ID AAW97177 standard; peptide; 113 AA.
XX
AC AAW97177;
XX
DT 06-MAY-1999 (first entry)
XX
DE Monoclonal antibody CC49 light chain variable region.
XX
KW Light chain variable region; human tumour-associated glycoprotein 72;
KW multivalent single-chain antibody; CC49 antibody; TAG-72; cancer.
XX
OS Mus sp.
XX
PN US5877291-A.
XX
PD 02-MAR-1999.
XX
PF 21-JUN-1994; 94US-00263911.
XX
PR 11-DEC-1992; 92US-00990263.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Gourlie BB, Mezes PS;
XX
WPI: 1999-189723/16.
DR N-PSDB; AAX15393.
XX
XX Multivalent single-chain antibody - specific for tumour-associated
PT glycoprotein 72.
XX
PS Claim 2; Col 37; 42pp; English.
XX
XX The present sequence represents the CC49 light chain variable region. The
CC sequence is used to construct a multivalent single-chain antibody
CC comprising two or more single-chain antibody fragments linked together by
CC a peptide linker (see AAW97179). Each single-chain antibody fragment
CC specifically binds to TAG-72 (human tumour-associated glycoprotein 72).
CC Multivalent single-chain antibodies can be conjugated with imaging or
CC therapeutic agents and used in the diagnosis and/or therapy of diseases
CC e.g. cancer
XX
SQ Sequence 113 AA;

Query Match          91.2%; Score 540; DB 2; Length 113;
Best Local Similarity 90.3%; Pred. No. 6.7e-37;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDLSAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIVMSQSPSLPVSIVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ESGVDPDRFSGSGGTDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ESGVDPDRFSGSGGTDTFTLTSSVKTEDLAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 ESGVDPDRFSGSGGTDTFTLTSSVKTEDLAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 18
AAW05759
ID AAY05759 standard; protein; 113 AA.
XX
AC AAY05759;
XX
DT 19-JUL-1999 (first entry)
XX
DE Anti-TAG-72 MAb CC49 VL domain.
XX
KW Multivalent single chain antibody; CC49; monoclonal antibody;
KW tumour associated glycoprotein 72; TAG-72; antigen; antibody engineering;
KW immunotherapy; therapy; immunodiagnosis; diagnosis.
XX
OS Mus musculus.
XX
PN US5892020-A.
XX
PD 06-APR-1999.
XX
PF 07-JUN-1995; 95US-00481006.
XX
PR 11-DEC-1992; 92US-00990263.
XX
PR 21-JUN-1994; 94US-00263911.
XX
PA (DOWC ) DOW CHEM CO.
XX
PI Mezes PS, Gourlie BB;
XX
WPI: 1999-253935/21.
DR N-PSDB; AAX25406.
XX
XX New sequences coding for a multivalent single chain antibody - useful for
PT identifying human tumour-associated glycoprotein 72, immunotherapy or
PT immunodiagnostics.
XX
PS Claim 1a; Col 18; 33pp; English.
XX
XX The present sequence represents the light chain variable region (VL) of
CC CC49, a murine monoclonal antibody specific to the human tumour-
CC associated glycoprotein 72 (TAG-72) antigen deposited as ATCC HB9459. The
CC invention discloses multivalent single chain antibodies composed of 2 or
CC more single chain antibodies and at least 1 peptide linker, each single
CC chain antibody having affinity for TAG-72 and comprising the CC49 VL
CC domain and the CC49 VH domain (see AAY05760). DNA sequences coding for
CC such multivalent single chain antibodies are claimed. The novel
CC antibodies can be used to identify TAG-72 in a sample, for immunotherapy
CC or immunodiagnostics. Two plasmids, p49LHLH and p49LHUL (see AAX25408 and
CC AAX25409), were constructed to produce single chain multivalent
CC antibodies. Both were transfected into Escherichia coli AG1 cells which
CC produced polypeptides of the sequence VL-L-VH-L-VL-L-VH (see AAY05762),
CC if containing p49LHLH, or VL-L-VH-L-VH-L-VL (see AAY05763), if containing
CC p49LHUL (where VL is the CC49 VL, VH is the CC49 VH and L is a linker
CC sequence). The small size of the multivalent single chain antibodies
CC allows their rapid removal from a system by capillary permeability
XX
SQ Sequence 113 AA;

Query Match          91.2%; Score 540; DB 2; Length 113;
Best Local Similarity 90.3%; Pred. No. 6.7e-37;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIVMSQSPDLSAVSLGERTVLTNCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 DIVMSQSPSLPVSIVGKVTLSCKSSQSLLYSGNQKNYLAWYQKQPGQSPKLLIYWASAR 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 ESGVDPDRFSGSGGTDTFTLTSSVQAEADVAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ESGVDPDRFSGSGGTDTFTLTSSVKTEDLAVVYCCQYYSYPLTFGAGTKLVK 113
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


KW tumour-associated glycoprotein-72; immunodetection; tumour cell;
XX surgical excision; disease status; cytostatic; CC49MuVK.
OS Mus sp.
XX
XX US2003013856-A1.
XX
XX 16-JAN-2003.
XX
XX 31-OCT-2001; 2001US-00040997.
XX
XX 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX
XX (ANDE/) ANDERSON W H K.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
PI WPI; 2003-401607/38.
XX
XX Claim 2; Fig 2; 29pp; English.
XX
XX The present invention relates to a novel humanised monoclonal antibody,
CC and its fragments which specifically binds tumour-associated glycoprotein
CC -72 (TAG-72), where the humanised monoclonal antibody is derived from a
CC murine monoclonal antibody (e.g. CC49) that binds TAG-72. The humanised
CC monoclonal antibody, and its fragments are useful for the treating and
CC detection of TAG-72 cancers which express TAG-72 (e.g. colon cancer). The
CC cancer is detected by the immunodetection of in vivo tumour cells, which
CC may be removed by surgical excision. The humanised monoclonal antibody of
CC the invention is useful as a immunodiagnostic agent both in vivo and in
CC vitro, and also for repeated monitoring of the disease status of a
CC patient. The present sequence represents murine monoclonal antibody CC49
CC VK (CC49MuVK)
XX
XX Sequence 113 AA;
XX
XX Query Match 91.2%; Score 540; DB 6; Length 113;
XX Best Local Similarity 90.3%; Pred. No. 6.7e-37;
XX Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
DB 1 DIVMSQSPSSLFVSVGKEVTLCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGSGTDTLTISVVOAEDVAVYVCQYYSVPLTFGAGTKLEK 113
DB 61 ESGVPRFSGSGSGTDTLTISVSVKTEDLAVYVCQYYSVPLTFGAGTKLVK 113
RESULT 22
ABU10146
ID ABU10146 standard; protein; 113 AA.
XX
XX AC ABU10146;
XX
XX 11-AUG-2003 (first entry)
XX
XX Murine TAG-72 antibody CC49 light chain variable region.
DE
XX Mouse; tumour-associated glycoprotein 72; TAG-72; antibody; CC49; cancer;
KW tumour; tumour imaging; serum clearance.
XX
XX Mus sp.

XX Location/Qualifiers
FH Key 24, 40
FT Region /label= CDR1
FT /note= "Complementarity determining region 1"
FT 56..62
FT Region /label= CDR2
FT /note= "Complementarity determining region 2"
FT 95..103
FT Region /label= CDR3
FT /note= "Complementarity determining region 3"
XX US2003013854-A1.
XX 16-JAN-2003.
XX
XX 31-OCT-2001; 2001US-00999021.
XX
XX 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX
XX (ANDE/) ANDERSON W H K.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
PI WPI; 2003-438920/41.
XX
XX Novel humanized monoclonal antibody which specifically binds tumor-
PT associated glycoprotein-72 useful for treating cancer and in vivo imaging
PT of tumors or cancer cells expressing the tumor-associated glycoprotein-
PT 72.
XX
XX Disclosure; Fig 4; 29pp; English.
XX
XX The invention relates to a humanised antibody (or its fragment) which
CC specifically binds tumour-associated glycoprotein 72 (TAG-72) (the
CC antibody or its fragment is derived from a murine antibody which
CC specifically binds TAG-72). The humanised antibody is useful for in vivo
CC treatment of cancer, by intravenously administering a radionuclide-
CC labelled antibody, detecting tumour cells using a radionuclide activity
CC probe, and removing the detected tumour cells by surgical excision. The
CC radionuclide is (125)I or (131)I. A composition containing the humanised
CC antibody is useful for in vivo treatment of a mammal having a TAG-72
CC expressing cancer. A composition containing the humanised antibody is
CC useful for in vitro immunodetection of TAG-72 expressing cancer cells,
CC where the antibody or its fragments of the composition are bound to a
CC solid support and also for in vivo tumour imaging. The humanised
CC antibodies have little or no reduced immunogenicity in humans over murine
CC and chimeric antibodies and have improved serum clearance and metabolic
CC properties. The antibodies can be used over prolonged time periods. The
CC present sequence represents the amino acid sequence of the murine TAG-72
CC antibody CC49 light chain variable region
XX
XX Sequence 113 AA;
XX
XX Query Match 91.2%; Score 540; DB 6; Length 113;
XX Best Local Similarity 90.3%; Pred. No. 6.7e-37;
XX Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
DB 1 DIVMSQSPSSLFVSVGKEVTLCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 60
QY 61 ESGVPRFSGSGSGTDTLTISVVOAEDVAVYVCQYYSVPLTFGAGTKLEK 113
DB 61 ESGVPRFSGSGSGTDTLTISVSVKTEDLAVYVCQYYSVPLTFGAGTKLVK 113

Query Match	91.2%	Score 540;	DB 6;	Length 113;
Best Local Similarity	90.3%	Pred. No. 6.7e-37;		
Matches 102; Conservative		7; Mismatches 4;	Indels 0;	Gaps 0;

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QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNKNYLAWYQOKPQSPKLLIYWASAR 60
Db 1 DIVMSQSPSSLPVSGEKVTLCKSSQSLLYSGNKNYLAWYQOKPQSPKLLIYWASAR 60
QY 61 ESGVPDRFSGSGGTDFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPDRFTGSGGTDFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

RESULT 25
ABU62757
ID ABU62757 standard; protein; 113 AA.
AC ABU62757;
XX
XX
DT 08-SEP-2003 (first entry)
XX
DE Murine monoclonal antibody CC49 variable light chain.
XX
KW Mouse; monoclonal antibody; CC49; variable kappa chain; cytostatic;
KW vaccine; humanised antibody; tumour-associated glycoprotein 72; TAG-72;
KW cancer; tumour.
XX
OS Mus musculus.
XX
PN US2003004318-A1.
XX
PD 02-JAN-2003.
XX
PF 31-OCT-2001; 2001US-00998817.
XX
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX
XX (ANDE//) ANDERSON W H K.
PA (TEMP//) TEMPEST P R.
PA (CARR//) CARR F J.
PA (HARR//) HARRIS W J.
PA (ARMO//) ARMOUR K.
XX
XX Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX WPI; 2003-491945/46.
XX
XX New humanized anti-tumor-associated glycoprotein (TAG)-72 antibodies or
PT antibody fragments, useful for treating cancers that express TAG-72, or
PT for in vivo or in vitro detection of cancer, e.g. in vivo imaging of
PT tumors or cancer cells.
XX
XX Claim 2; Fig 2; 41pp; English.
XX
XX The invention describes a humanised antibody or humanised antibody
CC fragment which specifically binds tumour-associated glycoprotein (TAG)-
CC 72. The humanised antibody or humanised antibody fragment is derived from
CC a murine antibody that binds TAG-72. The humanised anti-tumour-associated
CC glycoprotein (TAG)-72 antibodies or antibody fragments are useful for
CC treating cancers that express TAG-72, or for the in vivo or in vitro
CC detection of cancer, e.g. in vivo imaging of tumours or cancer cells that
CC express TAG-72. This is the amino acid sequence of mouse monoclonal
CC antibody CC49 variable light chain
XX
XX Sequence 113 AA;
XX
Query Match 91.2%; Score 540; DB 6; Length 113;
Best Local Similarity 90.3%; Pred. No. 6.7e-37;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERTVLTNCKSSQSLLYSGNKNYLAWYQOKPQSPKLLIYWASAR 60
Db 1 DIVMSQSPSSLPVSGEKVTLCKSSQSLLYSGNKNYLAWYQOKPQSPKLLIYWASAR 60
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QY 61 ESGVPDRFSGSGGTDFTLTISVQAEDVAVYCCQYYSYPLTFGAGTKLELK 113
Db 61 ESGVPDRFTGSGGTDFTLTISSVKTEDLAVYCCQYYSYPLTFGAGTKLVK 113

Search completed: July 25, 2005, 07:56:18
Job time : 122.969 secs
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OM protein - protein search, using sw model

Run on: July 25, 2005, 07:36:04 ; Search time 112.009 Seconds
(without alignments)
-521:183 Million cell updates/sec

Title: US-10-058-069-9_COPY_21_134

Perfect score: 592

Sequence: 1 DIVMSQSPDSLAISLGERVT.....QQYYSPLTFGAGTKLELKR 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532	89.9	114	1 KV4A HUMAN	P01625 homo sapien
2	526	88.9	134	1 KV4C HUMAN	P06314 homo sapien
3	512.5	86.6	133	1 KV4B HUMAN	P06313 homo sapien
4	492	83.1	255	2 Q6KB05	Q6kb05 mus musculus
5	484	81.8	121	1 KV4O HUMAN	P06312 homo sapien
6	479	80.9	109	1 KV4D HUMAN	P83593 homo sapien
7	418	70.6	114	1 KV1A MOUSE	P01632 mus musculus
8	405.5	68.5	109	2 Q9UL78	Q9ul78 homo sapien
9	400	67.6	108	2 Q9UL79	Q9ul79 homo sapien
10	398	67.2	111	1 KV3N MOUSE	P01666 mus musculus
11	397	67.1	108	1 KV1M HUMAN	P01605 homo sapien
12	397	67.1	108	2 Q9UL70	Q9ul70 homo sapien
13	395.5	66.8	109	1 KV3D HUMAN	P01622 homo sapien
14	395.5	66.8	129	1 KV3L HUMAN	P18135 homo sapien
15	395	66.7	149	1 KV5A MOUSE	P01633 mus musculus
16	394	66.6	240	2 Q6PIH6	Q6pih6 homo sapien
17	393	66.4	136	1 KV5B MOUSE	P01634 mus musculus
18	393	66.4	241	2 Q63ZX4	Q63zx4 mus musculus
19	392.5	66.3	129	1 KV3M HUMAN	P18136 homo sapien
20	392	66.2	236	2 Q723Y4	Q723y4 homo sapien
21	391.5	66.1	109	1 KV3B HUMAN	P01620 homo sapien
22	391	66.0	111	1 KV3U MOUSE	P01673 mus musculus
23	390	65.9	244	2 Q65ZC8	Q65zc8 homo sapien
24	389	65.7	111	1 KV3M MOUSE	P01665 mus musculus
25	389	65.7	236	2 Q6GMX8	Q6gmx8 homo sapien
26	388.5	65.6	109	1 KV3F HUMAN	P01624 homo sapien
27	388	65.5	111	1 KV3L MOUSE	P01664 mus musculus
28	388	65.5	111	1 KV3O MOUSE	P01667 mus musculus
29	387	65.4	108	1 KV1Y HUMAN	P80362 homo sapien
30	386.5	65.3	107	2 Q96SA9	Q96sa9 homo sapien
31	386.5	65.3	235	2 Q6GMV9	Q6gmv9 homo sapien

ALIGNMENTS

32	385.5	65.1	109	1 KV3E HUMAN	P01623 homo sapien
33	385	65.0	108	2 Q9UL83	Q9ul83 mus musculus
34	384	64.9	111	1 KV3S MOUSE	P01671 mus musculus
35	384	64.9	115	1 KV2A HUMAN	P01614 homo sapien
36	384	64.9	234	2 Q72473	Q72473 homo sapien
37	384	64.9	240	2 Q65ZC9	Q65zc9 homo sapien
38	383.5	64.8	109	2 Q9UL85	Q9ul85 homo sapien
39	383.5	64.8	239	2 Q8NEK0	Q8nek0 homo sapien
40	383	64.7	108	2 Q9UL77	Q9ul77 homo sapien
41	383	64.7	236	2 Q6PIL8	Q6pil8 homo sapien
42	382.5	64.6	108	1 KV3A HUMAN	P01619 homo sapien
43	382	64.5	236	2 Q6GMX9	Q6gmx9 homo sapien
44	381	64.4	129	1 KV1W HUMAN	P04431 homo sapien
45	381	64.4	236	2 Q6GMW1	Q6gmw1 homo sapien
46	380.5	64.3	107	2 Q9UL81	Q9ul81 homo sapien
47	380	64.2	108	1 KV1V HUMAN	P04430 mus musculus
48	380	64.2	111	1 KV3Q MOUSE	P01669 mus musculus
49	379.5	64.1	109	1 KV3G HUMAN	P04206 homo sapien
50	379.5	64.1	117	1 KV2E HUMAN	P06309 homo sapien
51	379	64.0	108	1 KV1K HUMAN	P01603 homo sapien
52	379	64.0	111	1 KV3K MOUSE	P01663 mus musculus
53	379	64.0	236	2 Q6GMX0	Q6gmx0 homo sapien
54	377.5	63.8	110	1 KV3P MOUSE	P01668 mus musculus
55	377.5	63.8	113	1 KV2D HUMAN	P01617 homo sapien
56	377.5	63.8	129	1 KV3H HUMAN	P04207 homo sapien
57	377.5	63.8	239	2 Q8TCD0	Q8tcd0 homo sapien
58	377	63.7	108	1 KV1H HUMAN	P01600 homo sapien
59	376.5	63.6	113	1 KV2B HUMAN	P01615 homo sapien
60	376.5	63.6	133	1 KV2F HUMAN	P06310 homo sapien
61	376.5	63.6	235	2 Q6GMW0	Q6gmw0 homo sapien
62	376	63.5	111	1 KV3H MOUSE	P01660 mus musculus
63	375.5	63.4	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
64	375	63.3	108	2 Q8VIJ0	Q8vijs mus musculus
65	374.5	63.3	113	1 KV2G MOUSE	P01631 mus musculus
66	374	63.2	108	1 KV1O HUMAN	P01607 homo sapien
67	374	63.2	128	1 KV5E MOUSE	P01637 mus musculus
68	374	63.2	236	2 Q6PIT5	Q6pit5 homo sapien
69	373	63.0	111	2 Q920E9	Q920e9 mus musculus
70	372.5	62.9	219	2 Q65ZC0	Q65zc0 mus musculus
71	372	62.8	108	1 KV1P HUMAN	P01670 mus musculus
72	372	62.8	111	1 KV3R MOUSE	P01670 mus musculus
73	371	62.7	108	1 KV1R HUMAN	P01610 homo sapien
74	371	62.7	111	2 Q81IU6	Q81iu6 mus musculus
75	371	62.7	236	2 Q6PIH7	Q6pih7 homo sapien
76	371	62.7	238	2 Q66JS7	Q66js7 mus musculus
77	370.5	62.6	113	1 KV2C MOUSE	P01628 mus musculus
78	370	62.5	112	1 KV3G MOUSE	P01659 mus musculus
79	370	62.5	236	2 Q6P5S8	Q6p5s8 homo sapien
80	369.5	62.4	109	2 Q9UL86	Q9ul86 homo sapien
81	369	62.3	99	2 Q9UL74	Q9j174 mus musculus
82	368	62.2	108	1 KV1B HUMAN	P01594 homo sapien
83	368	62.2	108	1 KV1L HUMAN	P01604 homo sapien
84	368	62.2	108	1 KV1S HUMAN	P01611 homo sapien
85	368	62.2	111	1 KV3J MOUSE	P01662 mus musculus
86	367	62.0	131	1 KV3I MOUSE	P01661 mus musculus
87	366	61.8	108	1 KV3V MOUSE	P01674 mus musculus
88	366	61.8	262	2 Q65Z11	Q65z11 mus musculus
89	365.5	61.7	235	2 Q6PFF2	Q6pfj2 homo sapien
90	364	61.5	112	1 KV1U HUMAN	P01613 homo sapien
91	363	61.3	128	1 KV1K HUMAN	P06311 homo sapien
92	363	61.3	132	1 KV3F MOUSE	P01558 mus musculus
93	361.5	61.1	112	2 Q6LEM8	Q6lem8 mus musculus
94	361.5	61.1	114	2 Q8XIF1	Q8xif1 mus musculus
95	361.5	61.1	243	2 Q6NTU5	Q6ntu5 xenopus lae
96	361	61.0	108	1 KV1C HUMAN	P01595 homo sapien
97	361	61.0	108	1 KV1E HUMAN	P01597 homo sapien
98	361	61.0	108	1 KV1G HUMAN	P01599 homo sapien
99	361	61.0	108	1 KV1Q HUMAN	P01609 homo sapien
100	361	61.0	111	1 KV3T MOUSE	P01672 mus musculus

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RESULT 1
KV4A_HUMAN STANDARD; PRT; 114 AA.
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE IG kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hillebrand N.;
RT "The primary structure of a monoclonal immunoglobulin-L-chain of
RL subgroup IV of the kappa type (Bence-Jones protein Len).";
RN Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1EEQ; X-ray; A/B=1-114.
DR PDB; 1EEU; X-ray; A/B=1-114.
DR PDB; 1EFQ; X-ray; A=1-114.
DR PDB; 1EK3; X-ray; A/B=1-114.
DR PDB; 1LVE; X-ray; @=1-114.
DR PDB; 3LVE; X-ray; @=1-114.
DR PDB; 5LVE; X-ray; A=1-114.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR Pfam; PF00047; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 113
FT DISULFID 23 94
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT STRAND 30 31
FT TURN 32 35
FT STRAND 36 37
FT STRAND 39 44
FT TURN 46 47
FT STRAND 51 55
FT TURN 56 58
FT STRAND 59 60
FT TURN 62 63
FT TURN 66 67
FT STRAND 68 73
FT TURN 74 75
FT STRAND 76 81
FT HELIX 86 88
FT STRAND 90 96
FT STRAND 103 104
FT STRAND 108 112
FT NON_TER 114
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SQ SEQUENCE 114 AA; 12640 MW; 0647FLD17F236485 CRC64;
Query Match 89.9%; Score 532; DB 1; Length 114;
Best Local Similarity 87.7%; Pred. No. 1.6e-47;
Matches 100; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVMSQSPDSLAVSLGERVTNCKSSQSLLYSGNQKNYLAWYQKPGSPKLLIYWASAR 60
DB 1 DIVMTQSPDSLAVSLGERATNCKSSQSLVYSSNKNYLAWYQKPGQPPKLLIYWASTR 60
QY 61 ESVGVDPRFSGSGGTFTLTISVQAEDVAVYVYCOQYVSYPLTGTGAGTKLEKR 114
DB 61 ESVGVDPRFSGSGGTFTLTISVQAEDVAVYVYCOQYVSYPLTGTGAGTKLEIKR 114
RESULT 2
KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RL probe.";
RN Nucleic Acids Res. 13:6531-6544(1985).
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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DR EMBL; X02990; CAA26733.1; -.
DR HSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DOMAIN 122 133 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;
Query Match 88.9%; Score 526; DB 1; Length 134;
Best Local Similarity 86.0%; Pred. No. 8.3e-47;
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Matches 98; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIVMSQPSLAVSLGERTVLTNCKSSQSLLYSGNKYLAQYQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLYSSDNKNYLAQYQKPGQSPKLLIYWASTR 80
QY 61 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKVEIKR 134

RESULT 3
KV40_HUMAN STANDARD; PRT; 133 AA.
ID Q6313;
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
DR EMBL; 20022; CAA77317.1; -
DR PIR; A01904; KAHUJI.
DR HSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region JI.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Framework-3.
FT DOMAIN 115 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 86.6%; Score 512.5; DB 1; Length 133;
Best Local Similarity 86.0%; Pred. NO. 2.1e-45;
Matches 98; Conservative 7; Mismatches 8; Indels 1; Gaps 1;
QY 1 DIVMSQPSLAVSLGERTVLTNCKSSQSLLYSGNKYLAQYQKPGQSPKLLIYWASAR 60
Db 21 DIVMTQSPDLSAVSLGERATINCKSSQSLYSSDNKNYLAQYQKPGQSPKLLIYWASTR 80
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QY 61 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKLELKR 114
Db 81 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKVEIKR 133

RESULT 4
Q6KB05 PRELIMINARY; PRT; 255 AA.
ID Q6KB05;
AC Q6KB05;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -
DR HSP; P01837; IKCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON_TER 1 1
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 83.1%; Score 492; DB 2; Length 255;
Best Local Similarity 84.1%; Pred. NO. 6e-43;
Matches 95; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIVMSQPSLAVSLGERTVLTNCKSSQSLLYSGNKYLAQYQKPGQSPKLLIYWASAR 60
Db 137 DIVMAQSPSSLSVSAKEVINSCKSSQLLSNRKNYLAQYQKPGQSPKLLIYGASTR 196
QY 61 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKLELKR 113
Db 197 ESGVDPFRSGSGTDFTLTSSVQAEADVAVYCOQYYSYPLTFGAGTKLEIK 249

RESULT 5
KV40_HUMAN STANDARD; PRT; 121 AA.
ID KV40_HUMAN
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN Name=IGKV4-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: There is only one Ig kappa V-IV gene.
CC -----
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DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01925; K4HU.
DR HSSP; P01625; ILVE.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 Ig kappa chain V-IV region.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DISULFID 115 121 Complementarity-determining-3.
FT NON TER 121 121 By similarity.
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 81.8%; Score 484; DB 1; Length 121;
Best Local Similarity 90.1%; Pred. No. 1.8e-42;
Matches 91; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGQSPKLLYWASAR 60
Db 21 DIVMTQSPDSLAVSLGERATINCRSSQSVLYSSNNKNYLAWYQKPGPPKLLIYWASTR 80

Qy 61 ESGVPDRFSGSGSGTDFTLTISVQAEDVAVVYCOQYYSYP 101
Db 81 ESGVPDRFSGSGSGTDFTLTISLQAEDVAVVYCOQYYSTP 121

RESULT 6
KV4D HUMAN STANDARD; PRT; 109 AA.
AC P83593;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180; DOI=10.1006/bbrc.1998.8515;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of Al-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
CC InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 40 Complementarity-determining-1.

FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 101 Complementarity-determining-3.
FT DOMAIN 102 109 Framework-4.
FT DISULFID 23 94 By similarity.
FT UNSURE 23 23
FT UNSURE 23 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 80.9%; Score 479; DB 1; Length 109;
Best Local Similarity 81.7%; Pred. No. 5.2e-42;
Matches 89; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQSLYSNGKNYLAWYQKPGQSPKLLYWASAR 60
Db 1 DIVMTQSPDSLAVSLGERATINCRSSQSVLYSSNNKNYLAWYQKPGQAPKLLFSWASTR 60

Qy 61 ESGVPDRFSGSGSGTDFTLTISVQAEDVAVVYCOQYYSYPLTFGAGTK 109
Db 61 ESGVPDRFSGSGSGTDFTLTIPGLQAEDVAVVYCOQYRIPYTFGQGA 109

RESULT 7
KVIA MOUSE STANDARD; PRT; 114 AA.
ID KVIA MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6788890;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains.";
RL J. Exp. Med. 153:1366-1370(1981).
CC -!- FUNCTION: Anti-phosphocholine antibody.

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CC EMBL; U29423; AAC00033.1; -.
DR PIR; A01915; KYMS7A.
DR HSSP; Q9ERZ9; 2AP2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IGV.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40 Complementarity-determining-1.
FT DOMAIN 41 55 Framework-2.
FT DOMAIN 56 62 Complementarity-determining-2.
FT DOMAIN 63 94 Framework-3.
FT DOMAIN 95 103 Complementarity-determining-3.
FT DOMAIN 104 113 Framework-4.
FT DISULFID 23 94 By similarity.
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;

[illegible]

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DR PIR; B01937; KWS83.
DR HSSP; P01665; 1QNZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 67.2%; Score 398; DB 1; Length 111;
Best Local Similarity 69.9%; Pred. No. 1.4e-33;
Matches 79; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 1 DIVLTQSPASLAVSLGQRTVITTCASQ-----SYNNYQKPGQFPKLLIYAASNL 58

Qy 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYQYYSYPLTFGAGTKLEK 113
Db 59 ESGIPARFSGSGGTDFLTINHPVEEDAAAYYCCQSNEDPLTFGAGTKLEK 111

RESULT 11
KV1M_KV1M HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human POM V-III kappa chain,
with which it shares certain idiotypic determinants.
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
DR PIR; A01871; KIHULY.
DR HSSP; P01607; 1BWV.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.

FT PIR; B01937; KWS83.
FT HSSP; P01665; 1QNZ.
FT InterPro; IPR007110; Ig-like.
FT InterPro; IPR003596; Ig_v.
FT Pfam; PF00047; Ig; 1.
FT SMART; SM00406; IGV; 1.
FT PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 67.1%; Score 397; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.8e-33;
Matches 76; Conservative 15; Mismatches 17; Indels 6; Gaps 1;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 1 DIQMTQSPSSLSASVGRVITTCASQ-----NNVAYLAWYQKPGKPLIYGASTR 54

Qy 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYQYYSYPLTFGAGTKLEK 114
Db 55 EAGVPSRFSGSGGTDFLTITSSLPEDIATYYCQYNWNPPTFGQGTKEVKR 108

RESULT 12
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 67.1%; Score 397; DB 2; Length 108;
Best Local Similarity 67.5%; Pred. No. 1.8e-33;
Matches 77; Conservative 13; Mismatches 18; Indels 6; Gaps 1;

Qy 1 DIVMSQSPDSLAVSLGERVTLNCKSSQLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 60
Db 1 DIQMTQSPSSLSASVGRVITTCASQGI-----SNLYAWYQKPGKPKSLIYAASLT 54

Qy 61 ESGVDPDRFSGSGGTDFLTITSSVQAEADVAVYQYYSYPLTFGAGTKLEK 114
Db 55 QSGVPSRFSGSGGTDFLTITSSLPEDIATYYCQYNWNPPTFGQGTKEIKR 108

RESULT 13
KV3D_KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-III region Tl.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FT	DOMAIN	56	70	Framework-2.
FT	DOMAIN	71	77	Complementarity-determining-2.
FT	DOMAIN	78	109	Framework-3.
FT	DOMAIN	110	118	Complementarity-determining-3.
FT	DOMAIN	119	129	JK1 segment.
FT	DISULFID	43	109	By similarity.
FT	NON TER	129	129	
SQ	SEQUENCE	129 AA;	14070 MW;	7395528EA2BB74D6 CRC64;

Query Match	66.3%;	Score 392.5;	DB 1;	Length 129;
Best Local Similarity	64.9%;	Pred. No. 6.4e-33;		
Matches	74;	Conservative	20;	Mismatches 15; Indels 5; Gaps 1;

QY	1	DIYWSQPSDLAVSLGSRVTNLKSSQSLLSYGNQKNYLAWYQKQPSKLLIY	WASAR	60
DB	21	EIVLTSPGTLSPGSRATLSRASQSV----	SSSYLAWYQKQPSKLLIY	GASSR 75
QY	61	ESGVPRFSGSGGTDFTLTSSVQADVAVYVCOQYVSPYPLTFGAGTKLE	KR	114
DB	76	ATGIPDFSGSGGTDFTLTISRLPDXDFAVYVCOQYSSSPWTFGGTKV	EIKR	129

RESULT 20				
Q723Y4				
ID	Q723Y4	PRELIMINARY;	PRT;	236 AA.
AC	Q723Y4			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Skeletal Muscle;			
RC	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalka U., Smillus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Skeletal Muscle;			
RA	Strausberg R.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC005332; AAH05332.1; -;			
DR	HSSP; P01834; 1HEZ.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig_VHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_VHC; UNKNOWN 1.			


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DE Ig kappa chain V-III region PC 2485/PC 4039.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RP
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790 (1978).
CC -!- MISCELLANEOUS: The PC 4285 and PC 4039 sequences are identical.
DR HSP; P01665; IONZ.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Complementarity-determining-2.
FT DOMAIN 54 60 Complementarity-determining-3.
FT DOMAIN 61 92 Complementarity-determining-4.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; BF38C59AA7858467 CRC64;

Query Match 66.0%; Score 391; DB 1; Length 111;
Best Local Similarity 68.1%; Pred. No. 7.7e-33;
Matches 77; Conservative 14; Mismatches 20; Indels 2; Gaps 1;

QY 1 DIVMSQPSDLAVSLGERTVLTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASAR 60
DB 1 DIVLTQSPASLASVIGQRATISCRASKSVSTSG--YSYMHYQKPGQPKLLIYLAASL 58

QY 61 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEIK 113
DB 59 ESGVDPFRSGSGTGDTLTINIQVEEDAATYICQHSRELPLTFGAGTKLEIK 111

RESULT 23
Q652C8 PRELIMINARY; PRT; 244 AA.
ID Q652C8 PRELIMINARY; PRT; 244 AA.
AC Q652C8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name-scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=97362799; PubMed=9219263;
RX Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631 (1997).
DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON_TER 1 1

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FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 65.9%; Score 390; DB 2; Length 244;
Best Local Similarity 63.2%; Pred. No. 2.4e-32;
Matches 72; Conservative 19; Mismatches 17; Indels 6; Gaps 1;

QY 1 DIVMSQPSDLAVSLGERTVLTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASAR 60
DB 137 DIQTQSPSTLSASIGDRVTITCRASEGIYH-----WLAWYQKPGKAPKFLIYKASSL 190

QY 61 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKR 114
DB 191 ASGARPSRFGSGSGTGDTLTITSSLPQDFATYICQYSNYPLTFGGGKLEIKR 244

RESULT 24
KV3M MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45; Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_SEQUENCE.
RP MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
  diversity.";
RL Nature 276:785-790 (1978).
DR PIR; A01937; KVM843.
DR PDB; 1QNZ; NMR; L=1-111.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Complementarity-determining-2.
FT DOMAIN 54 60 Complementarity-determining-3.
FT DOMAIN 61 92 Complementarity-determining-4.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DISULFID 23 92 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 65.7%; Score 389; DB 1; Length 111;
Best Local Similarity 67.3%; Pred. No. 1.2e-32;
Matches 76; Conservative 14; Mismatches 21; Indels 2; Gaps 1;

QY 1 DIVMSQPSDLAVSLGERTVLTNCKSSQSLLYSGNKNYLAWYQKPGQPKLLIYWASAR 60
DB 1 DIVLTQSPASLASVIGQRATISCRASKSVSDYDGD--SYNNWYQKPGQPKLLIYAASNL 58

QY 61 ESGVDPFRSGSGTGDTLTITSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEIK 113
DB 59 ESGIPARPSGSGTGDTLTINHPVEEDAATYICQSNEDPTFFSGTKLEIK 111

RESULT 25
Q6GMX8 PRELIMINARY; PRT; 236 AA.
ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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Search completed: July 25, 2005, 08:00:08
Job time : 114.009 secs